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From: Whiteman, Brian  
Sent: Monday, June 27, 2005 8:06 AM  
To: STIC-Biotech/ChemLib  
Subject: sequence search

10/057,136 Schlom et al. EFD 1/25/02

SEQ ID NOs: 1, 2 and 4-12

- 1) oligonucleotide search against interference databases
- 2) oligonucleotide search against public databases

Thank you,

Brian Whiteman  
Remsen, 2D14  
mail box 2C18  
Patent Examiner - Art Unit 1635  
United States Patent and Trademark Office  
(571) 272-0764

1 aa 20

2 na 60

4

5

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7

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9

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11

12

60

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Searcher: \_\_\_\_\_  
Searcher Phone: 2-\_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date Completed: \_\_\_\_\_  
Searcher Prep/Rev. Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*  
Type of Search

NA#: \_\_\_\_\_ AA#: \_\_\_\_\_  
Interference: \_\_\_\_\_ SPDI: \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure#: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*  
Vendors and cost where applicable  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other(Specify): \_\_\_\_\_

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 29, 2005, 23:23:45 ; Search time 230.7 Seconds

(without alignments)

1625.622 Million cell updates/sec

Title: US-10-057-136-4

Perfect score: 60

Sequence: 1 ggcagtgactgcaccacggc.....ctgatacaagacctgcacct 60

Scoring table: OLIGO NUC

Gapop 60.0, Gapext 60.0

Searched: 6067389 seqs, 3125258755 residues

Word size : 0

Total number of hits satisfying chosen parameters: 12134778

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications NA:\*

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- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq.\*
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- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq.\*
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- 9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq.\*
- 10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq.\*
- 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq.\*
- 12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq.\*
- 13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq.\*
- 14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq.\*
- 15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq.\*
- 16: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq.\*
- 17: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq.\*
- 18: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq.\*
- 19: /cgn2\_6/ptodata/1/pubpna/US10G\_PUBCOMB.seq.\*
- 20: /cgn2\_6/ptodata/1/pubpna/US10H\_PUBCOMB.seq.\*
- 21: /cgn2\_6/ptodata/1/pubpna/US10I\_PUBCOMB.seq.\*
- 22: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq.\*
- 23: /cgn2\_6/ptodata/1/pubpna/US11A\_PUBCOMB.seq.\*
- 24: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq.\*
- 25: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*
- 26: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	60	100.0	60	14	US-10-057-136-4
2	60	100.0	2297	17	US-10-406-317-41
3	17	28.3	746	18	US-10-424-599-119193
4	17	28.3	863	18	US-10-424-599-131807
5	17	28.3	891	17	US-10-282-122A-37454
6	17	28.3	1756	17	US-10-282-122A-23378
7	17	28.3	1768	17	US-10-282-122A-19753

c	8	17	28.3	1805	18	US-10-424-599-131806	Sequence 131806, A
c	9	16	26.7	201	21	US-10-741-600-56574	Sequence 56574, A
c	10	16	26.7	382	19	US-10-437-963-75101	Sequence 75101, A
c	11	16	26.7	557	9	US-09-878-178-919	Sequence 919, App
c	12	16	26.7	557	13	US-10-046-935-919	Sequence 919, App
c	13	16	26.7	557	14	US-10-146-502-919	Sequence 919, App
c	14	16	26.7	816	15	US-10-156-761-5190	Sequence 5190, App
c	15	16	26.7	1089	17	US-10-369-493-44330	Sequence 44330, A
c	16	16	26.7	1301	9	US-09-974-300-6140	Sequence 6140, App
c	17	16	26.7	1554	17	US-10-282-122A-17757	Sequence 17757, A
c	18	16	26.7	1752	17	US-10-282-122A-41450	Sequence 41450, A
c	19	16	26.7	4167	17	US-10-282-122A-33967	Sequence 33967, A
c	20	16	26.7	15251	19	US-10-451-467A-669	Sequence 669, App
c	21	16	26.7	65300	21	US-10-741-600-17776	Sequence 17776, A
c	22	16	26.7	175189	21	US-10-741-600-17738	Sequence 17738, A
c	23	16	26.7	9025608	15	US-10-156-761-1	Sequence 1, Appli
c	24	15	25.0	20	21	US-10-831-901A-9924	Sequence 9924, Ap
c	25	15	25.0	20	21	US-10-831-901A-9925	Sequence 9925, Ap
c	26	15	25.0	20	21	US-10-831-901A-9926	Sequence 9926, Ap
c	27	15	25.0	20	21	US-10-831-901A-9927	Sequence 9927, Ap
c	28	15	25.0	20	21	US-10-831-901A-9928	Sequence 9928, Ap
c	29	15	25.0	20	21	US-10-831-901A-9929	Sequence 9929, Ap
c	30	15	25.0	100	17	US-10-242-535A-366	Sequence 366, App
c	31	15	25.0	100	18	US-10-085-783A-366	Sequence 366, App
c	32	15	25.0	201	21	US-10-741-600-32304	Sequence 32304, A
c	33	15	25.0	201	21	US-10-741-600-32310	Sequence 32310, A
c	34	15	25.0	201	21	US-10-741-600-32312	Sequence 32312, A
c	35	15	25.0	261	17	US-10-282-122A-36430	Sequence 36430, A
c	36	15	25.0	275	17	US-10-305-720-341	Sequence 341, App
c	37	15	25.0	346	18	US-10-424-599-28755	Sequence 28755, A
c	38	15	25.0	434	20	US-10-425-115-60507	Sequence 60507, A
c	39	15	25.0	448	9	US-09-796-632-8159	Sequence 8159, Ap
c	40	15	25.0	448	14	US-10-040-862-8159	Sequence 8159, Ap
c	41	15	25.0	448	17	US-10-057-475B-8159	Sequence 8159, Ap
c	42	15	25.0	448	17	US-10-154-884B-8159	Sequence 8159, Ap
c	43	15	25.0	448	19	US-10-764-324-8159	Sequence 8159, Ap
c	44	15	25.0	456	17	US-10-369-493-24810	Sequence 24810, A
c	45	15	25.0	477	10	US-09-814-353-16515	Sequence 16515, A

#### ALIGNMENTS

#### RESULT 1

US-10-057-136-4  
; Sequence 4, Application US/10057136  
; Publication No. US20030021770A1  
; GENERAL INFORMATION:  
; APPLICANT: SCHLOM, JEFFREY  
; APPLICANT: KANTOR, JUDITH  
; APPLICANT: KUFE, DONALD  
; APPLICANT: PANICALI, DENNIS  
; APPLICANT: GRITZ, LINDA  
; TITLE OF INVENTION: RECOMBINANT POX VIRUS FOR IMMUNIZATION AGAINST MUC1  
; FILE OF INVENTION: 700953/47113C  
; FILE REFERENCE: 700953/47113C  
; CURRENT FILING DATE: 2002-01-25  
; PRIOR APPLICATION NUMBER: 09/366,670  
; PRIOR FILING DATE: 1999-08-03  
; PRIOR APPLICATION NUMBER: PCT/US98/03693  
; PRIOR FILING DATE: 1998-02-24  
; PRIOR APPLICATION NUMBER: 60/038,253  
; PRIOR FILING DATE: 1997-02-24  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 60  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-057-136-4

Query Match 100.0% Score 60; DB 14; Length 60;

Best Local Similarity 100.0%; Pred. No. 4e-22;  
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGCAGTACTGCACACCGGCACATGGCGTAACATCAGACCTGTATACAAGACCTGCACCT 60  
Db 1 GGCAGTACTGCACACCGGCACATGGCGTAACATCAGACCTGTATACAAGACCTGCACCT 60

RESULT 2  
US-10-406-317-41  
; Sequence 41, Application US/10406317  
; Publication No. US20040019195A1  
; GENERAL INFORMATION:  
; APPLICANT: Schlom, Jeffrey;  
; APPLICANT: Hodge, James;  
; APPLICANT: Panicali, Dennis  
; TITLE OF INVENTION: A recombinant vector expressing multiple constimulatory  
; TITLE OF INVENTION: molecules and uses thereof  
; FILE REFERENCE: 38163-0189  
; CURRENT APPLICATION NUMBER: US/10/406,317  
; CURRENT FILING DATE: 2003-04-04  
; PRIOR APPLICATION NUMBER: US/09/856,988  
; PRIOR FILING DATE: 2001-05-30  
; PRIOR APPLICATION NUMBER: PCT/US99/26866  
; PRIOR FILING DATE: 1999-11-12  
; PRIOR APPLICATION NUMBER: 60/111,582  
; PRIOR FILING DATE: 1998-12-09  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 41  
; LENGTH: 2297  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: VECTOR  
US-10-406-317-41

Query Match 100.0%; Score 60; DB 17; Length 2297;  
Best Local Similarity 100.0%; Pred. No. 3e-22;  
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGCAGTACTGCACACCGGCACATGGCGTAACATCAGACCTGTATACAAGACCTGCACCT 60  
Db 406 GGCAGTACTGCACACCGGCACATGGCGTAACATCAGACCTGTATACAAGACCTGCACCT 465

RESULT 3  
US-10-424-599-119193/c  
; Sequence 119193, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 119193  
; LENGTH: 746  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(746)  
; OTHER INFORMATION: unsure at all n locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_7863C.1  
US-10-424-599-119193

Query Match 28.3%; Score 17; DB 18; Length 746;  
Best Local Similarity 100.0%; Pred. No. 29;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 35 CAGCACCTGTATACAAGA 51  
Db 74 CAGCACCTGTATACAAGA 58

RESULT 4  
US-10-424-599-131807/c  
; Sequence 131807, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 131807  
; LENGTH: 863  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_90029C.1  
US-10-424-599-131807

Query Match 28.3%; Score 17; DB 18; Length 863;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 35 CAGCACCTGTATACAAGA 51  
Db 766 CAGCACCTGTATACAAGA 750

RESULT 5  
US-10-282-122A-37454/c  
; Sequence 37454, Application US/10282122A  
; Publication No. US20040029129A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Liangsu  
; APPLICANT: Zamudio, Carlos  
; APPLICANT: Malone, Cheryl  
; APPLICANT: Haeelbeck, Robert  
; APPLICANT: Ohlsen, Kari  
; APPLICANT: Zyskind, Judith  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John  
; APPLICANT: Carr, Grant  
; APPLICANT: Yamamoto, Robert  
; APPLICANT: Forsyth, R.  
; APPLICANT: Xu, H.  
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
; FILE REFERENCE: ELITRA 034A  
; CURRENT APPLICATION NUMBER: US/10/282,122A  
; CURRENT FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/230,335  
; PRIOR FILING DATE: 2000-09-06  
; PRIOR APPLICATION NUMBER: 60/230,347  
; PRIOR FILING DATE: 2000-09-09



; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/267,636  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 78614  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 37454  
; LENGTH: 891  
; TYPE: DNA  
; ORGANISM: Streptococcus pneumoniae  
US-10-282-122A-37454

Query Match 28.3%; Score 17; DB 17; Length 891;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 40 CCTGATACAGACCTGC 56  
Db 224 CCTGATACAGACCTGC 208

RESULT 6  
US-10-282-122A-23378/c  
; Sequence 23378, Application US/10282122A  
; Publication No. US20040029129A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Liangsu  
; APPLICANT: Zamudio, Carlos  
; APPLICANT: Malone, Cheryl  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari  
; APPLICANT: Zyskind, Judith  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John  
; APPLICANT: Carr, Grant  
; APPLICANT: Yamamoto, Robert  
; APPLICANT: Forsyth, R.  
; APPLICANT: Xu, H.  
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
; FILE REFERENCE: ELITRA 034A  
; CURRENT APPLICATION NUMBER: US/10/282,122A  
; CURRENT FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/230,335  
; PRIOR FILING DATE: 2000-09-06  
; PRIOR APPLICATION NUMBER: 60/230,347  
; PRIOR FILING DATE: 2000-09-09  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/267,636  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 78614  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 23378

; LENGTH: 1756  
; TYPE: DNA  
; ORGANISM: Klebsiella pneumoniae  
US-10-282-122A-23378

Query Match 28.3%; Score 17; DB 17; Length 1756;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 5 GTACTGCACCACCGCA 21  
Db 663 GTACTGCACCACCGCA 647

RESULT 7  
US-10-282-122A-19753/c  
; Sequence 19753, Application US/10282122A  
; Publication No. US20040029129A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Liangsu  
; APPLICANT: Zamudio, Carlos  
; APPLICANT: Malone, Cheryl  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari  
; APPLICANT: Zyskind, Judith  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John  
; APPLICANT: Carr, Grant  
; APPLICANT: Yamamoto, Robert  
; APPLICANT: Forsyth, R.  
; APPLICANT: Xu, H.  
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
; FILE REFERENCE: ELITRA 034A  
; CURRENT APPLICATION NUMBER: US/10/282,122A  
; CURRENT FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/230,335  
; PRIOR FILING DATE: 2000-09-06  
; PRIOR APPLICATION NUMBER: 60/230,347  
; PRIOR FILING DATE: 2000-09-09  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/267,636  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 78614  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 19753  
; LENGTH: 1768  
; TYPE: DNA  
; ORGANISM: Enterobacter cloacae  
US-10-282-122A-19753

Query Match 28.3%; Score 17; DB 17; Length 1768;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 5 GTACTGCACCACCGCA 21  
Db 667 GTACTGCACCACCGCA 651

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RESULT 8
US-10-424-599-131806/c
; Sequence 131806, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 131806
; LENGTH: 1805
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(1805)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_90028C.1
US-10-424-599-131806

Query Match      28.3%; Score 17; DB 18; Length 1805;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      35 CAGCACCCTGATACAGA 51
      |||||
Db      760 CAGCACCCTGATACAGA 744

RESULT 9
US-10-741-600-56574
; Sequence 56574, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C0001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56574
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-56574

Query Match      26.7%; Score 16; DB 21; Length 201;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      40 CCTGATACAGACCTG 55
      |||||
Db      44 CCTGATACAGACCTG 59

RESULT 10
US-10-437-963-75101/c
; Sequence 75101, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
```

```
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 75101
; LENGTH: 382
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_75220C.1
US-10-437-963-75101

Query Match      26.7%; Score 16; DB 19; Length 382;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      40 CCTGATACAGACCTG 55
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Db      120 CCTGATACAGACCTG 105

RESULT 11
US-09-878-178-919
; Sequence 919, Application US/09878178
; Patent No. US20020177552A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.527
; CURRENT APPLICATION NUMBER: US/09/878,178
; CURRENT FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 2237
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 919
; LENGTH: 557
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-878-178-919

Query Match      26.7%; Score 16; DB 9; Length 557;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      45 TACAAGACCTGCACCT 60
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Db      541 TACAAGACCTGCACCT 556

RESULT 12
US-10-046-935-919
; Sequence 919, Application US/10046935
; Publication No. US20020156011A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Secrist, Heather
; APPLICANT: Wang, Aijun
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.527C1
; CURRENT APPLICATION NUMBER: US/10/046,935
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 2239
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 919
; LENGTH: 557
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-046-935-919

Query Match      26.7%; Score 16; DB 13; Length 557;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 45 TACAAGACCTGCACCT 60
|||||
Db 541 TACAAGACCTGCACCT 556

RESULT 13
US-10-146-502-919
; Sequence 919, Application US/10146502
; Publication No. US20030069180A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Secrist, Heather
; APPLICANT: Wang, Aijun
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.527C2
; CURRENT APPLICATION NUMBER: US/10/146.502
; CURRENT FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2241
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 919
; LENGTH: 557
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-146-502-919

Query Match      26.7%; Score 16; DB 14; Length 557;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 45 TACAAGACCTGCACCT 60
|||||
Db 541 TACAAGACCTGCACCT 556

RESULT 14
US-10-156-761-5190/c
; Sequence 5190, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156.761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 5190
; LENGTH: 816
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis

; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(816)
US-10-156-761-5190

Query Match      26.7%; Score 16; DB 15; Length 816;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CTGCACCCACCGGCACA 23
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Db 30 CTGCACCCACCGGCACA 15

RESULT 15
US-10-369-493-44330/c
; Sequence 44330, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369.493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 44330
; LENGTH: 1089
; TYPE: DNA
; ORGANISM: Rhodospseudomonas palustris
US-10-369-493-44330

Query Match      26.7%; Score 16; DB 17; Length 1089;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GTACTGCACCCACCGGC 20
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Db 669 GTACTGCACCCACCGGC 654

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Job time : 278.7 secs
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OM nucleic - nucleic search, using sw model

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(without alignments)  
1917.512 Million cell updates/sec

Title: US-10-057-136-4

Perfect score: 60

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Gapop 60.0 , Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

- Database : Issued Patents NA.\*
- 1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq.\*
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  - 5: /cgn2\_6/ptodata/1/ina/pCTUS\_COMB.seq.\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	17	28.3	1206	4	US-09-489-039A-1114
2	17	28.3	1770	4	US-09-489-039A-1224
3	16	26.7	474	4	US-09-248-796A-4236
4	16	26.7	543	4	US-09-270-767-4523
5	16	26.7	543	4	US-09-270-767-19805
6	16	26.7	601	4	US-09-949-016-136647
7	16	26.7	696	4	US-09-902-540-4831
8	16	26.7	26559	4	US-09-902-540-1237
9	16	26.7	162914	4	US-09-949-016-15578
10	15	25.0	93	4	US-09-270-767-5702
11	15	25.0	93	4	US-09-270-767-20984
12	15	25.0	275	4	US-09-016-434-341
13	15	25.0	421	4	US-09-621-976-2831
14	15	25.0	441	4	US-09-902-540-4058
15	15	25.0	498	4	US-09-252-991A-7343
16	15	25.0	546	3	US-09-643-597-129
17	15	25.0	546	4	US-09-480-884A-129
18	15	25.0	546	4	US-09-542-615A-129
19	15	25.0	546	4	US-09-606-421B-129
20	15	25.0	546	4	US-09-221-107-129
21	15	25.0	546	4	US-09-466-396A-129
22	15	25.0	546	4	US-09-476-496A-129
23	15	25.0	546	4	US-09-630-940B-129
24	15	25.0	546	4	US-09-285-479-129
25	15	25.0	601	4	US-09-949-016-80046
26	15	25.0	601	4	US-09-949-016-80047
27	15	25.0	601	4	US-09-949-016-131978

28	15	25.0	601	4	US-09-949-016-132047
c 29	15	25.0	601	4	US-09-949-016-149501
c 30	15	25.0	601	4	US-09-949-016-149502
31	15	25.0	681	4	US-09-252-991A-7273
32	15	25.0	792	4	US-09-902-540-8829
33	15	25.0	945	4	US-09-252-991A-7152
34	15	25.0	1043	4	US-09-270-767-1158
35	15	25.0	1043	4	US-09-270-767-16440
c 36	15	25.0	1074	4	US-09-614-221A-174
c 37	15	25.0	1174	2	US-08-793-410-9
c 38	15	25.0	1279	4	US-09-902-540-6180
c 39	15	25.0	1329	4	US-09-252-991A-13223
c 40	15	25.0	1533	4	US-09-949-016-4452
c 41	15	25.0	1959	4	US-09-902-540-313
c 42	15	25.0	2012	2	US-08-555-568B-16
c 43	15	25.0	2012	3	US-09-519-223-16
c 44	15	25.0	2012	4	US-09-927-180-16
c 45	15	25.0	2109	2	US-08-555-568B-20

ALIGNMENTS

RESULT 1  
US-09-489-039A-1114  
; Sequence 1114, Application US/09489039A  
; Patent No. 6610836  
; GENERAL INFORMATION:  
; APPLICANT: Gary Breton et. al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
; FILE REFERENCE: 2709.2004001  
; CURRENT APPLICATION NUMBER: US/09/489,039A  
; CURRENT FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: US 60/117,747  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 14342  
; SEQ ID NO 1114  
; LENGTH: 1206  
; TYPE: DNA  
; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-1114

Query Match 28.3%; Score 17; DB 4; Length 1206;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	5	GTACTGCACCACCGCA	21
Db	1132	GTACTGCACCACCGCA	1148

RESULT 2  
US-09-489-039A-1224/c  
; Sequence 1224, Application US/09489039A  
; Patent No. 6610836  
; GENERAL INFORMATION:  
; APPLICANT: Gary Breton et. al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
; FILE REFERENCE: 2709.2004001  
; CURRENT APPLICATION NUMBER: US/09/489,039A  
; CURRENT FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: US 60/117,747  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 14342  
; SEQ ID NO 1224  
; LENGTH: 1770  
; TYPE: DNA  
; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-1224

Query Match 28.3%; Score 17; DB 4; Length 1770;

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Best Local Similarity 100.0%; Pred. No. 11;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GTACTGCACCGCGCA 21
    |||||
Db 639 GTACTGCACCGCGCA 623

RESULT 3
US-09-248-796A-4236
; Sequence 4236, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 4236
; LENGTH: 474
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-4236

Query Match 26.7%; Score 16; DB 4; Length 474;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 GTAACATCAGCACCTG 43
    |||||
Db 130 GTAACATCAGCACCTG 145

RESULT 4
US-09-270-767-4523/c
; Sequence 4523, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4523
; LENGTH: 543
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-4523

Query Match 26.7%; Score 16; DB 4; Length 543;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 CACCACCGGCACATGG 26
    |||||
Db 238 CACCACCGGCACATGG 223

RESULT 5
US-09-270-767-19805/c
; Sequence 19805, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
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; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19805
; LENGTH: 543
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-19805

Query Match 26.7%; Score 16; DB 4; Length 543;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 CACCACCGGCACATGG 26
    |||||
Db 238 CACCACCGGCACATGG 223

RESULT 6
US-09-949-016-136647/c
; Sequence 136647, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 136647
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-136647

Query Match 26.7%; Score 16; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 34 TCAGCACCTGATACAA 49
    |||||
Db 150 TCAGCACCTGATACAA 135

RESULT 7
US-09-902-540-4831/c
; Sequence 4831, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 4831
; LENGTH: 696
; TYPE: DNA
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; ORGANISM: Myxococcus xanthus
US-09-902-540-4831

Query Match      26.7%; Score 16; DB 4; Length 696;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GCACACCGGCACATG 25
Db 514 GCACACCGGCACATG 499

RESULT 8
US-09-902-540-1237
; Sequence 1237, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1237
; LENGTH: 26659
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-1237

Query Match      26.7%; Score 16; DB 4; Length 26659;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GCACACCGGCACATG 25
Db 6906 GCACACCGGCACATG 6921

RESULT 9
US-09-949-016-15578
; Sequence 15578, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15578
; LENGTH: 162914
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(162914)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15578

Query Match      26.7%; Score 16; DB 4; Length 162914;

; ORGANISM: Drosophila melanogaster
US-09-270-767-5702
; Sequence 5702, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5702
; LENGTH: 93
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-5702

Query Match      25.0%; Score 15; DB 4; Length 93;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CTGCACACCGGCAC 22
Db 34 CTGCACACCGGCAC 48

RESULT 11
US-09-270-767-20984
; Sequence 20984, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20984
; LENGTH: 93
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-20984

Query Match      25.0%; Score 15; DB 4; Length 93;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CTGCACACCGGCAC 22
Db 34 CTGCACACCGGCAC 48

RESULT 12
US-09-016-434-341/c
; Sequence 341, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
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Query Match      25.0%; Score 15; DB 4; Length 421;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels
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Qy 8 CTGCACCAACCGGCAC 22  
Db 420 CTGCACCAACCGGCAC 406

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 29, 2005, 23:23:45 ; Search time 230.7 Seconds  
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1625.622 Million cell updates/sec

Title: US-10-057-136-6

Perfect score: 60

Sequence: 1 gggtaacagctctccgcg.....cagatactgcccagctcca 60

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Total number of hits satisfying chosen parameters: 12134778

Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

Database : Published Applications NA:\*

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq.\*
- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq.\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq.\*
- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq.\*
- 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq.\*
- 6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq.\*
- 7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq.\*
- 8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq.\*
- 9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq.\*
- 10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq.\*
- 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq.\*
- 12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq.\*
- 13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq.\*
- 14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq.\*
- 15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq.\*
- 16: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq.\*
- 17: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq.\*
- 18: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq.\*
- 19: /cgn2\_6/ptodata/1/pubpna/US10G\_PUBCOMB.seq.\*
- 20: /cgn2\_6/ptodata/1/pubpna/US10H\_PUBCOMB.seq.\*
- 21: /cgn2\_6/ptodata/1/pubpna/US10I\_PUBCOMB.seq.\*
- 22: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq.\*
- 23: /cgn2\_6/ptodata/1/pubpna/US11A\_PUBCOMB.seq.\*
- 24: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq.\*
- 25: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*
- 26: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	DB ID	Description
1	60	100.0	60	US-10-057-136-6
2	60	100.0	2297	Sequence 6, Appli
3	20	33.3	201	Sequence 41, Appl
4	20	33.3	201	Sequence 3612, Ap
5	20	33.3	201	Sequence 3628, Ap
6	20	33.3	201	Sequence 3676, Ap
7	20	33.3	453	Sequence 1712, Ap

Sequence 517, App

Query Match 100.0%; Score 60; DB 14; Length 60;

c 8	20	33.3	1405	21	US-10-741-600-65	Sequence 65, Appl
c 9	20	33.3	2655	21	US-10-741-600-62	Sequence 62, Appl
c 10	20	33.3	2659	21	US-10-741-600-61	Sequence 61, Appl
c 11	20	33.3	2747	21	US-10-741-600-17923	Sequence 17923, A
c 12	20	33.3	27875	21	US-10-741-600-17578	Sequence 17578, A
c 13	18	30.0	1228	19	US-10-437-963-97051	Sequence 97051, A
c 14	18	30.0	2493	19	US-10-437-963-97047	Sequence 97047, A
c 15	18	30.0	3899	9	US-09-735-367B-5	Sequence 5, Appli
c 16	18	30.0	6504	9	US-09-735-367B-9	Sequence 9, Appli
c 17	18	30.0	6504	9	US-09-735-367B-9	Sequence 9, Appli
c 18	18	30.0	6504	21	US-10-843-641A-8300	Sequence 8300, Ap
c 19	18	30.0	6878	9	US-09-735-367B-1	Sequence 1, Appli
c 20	17	28.3	230	20	US-10-357-930-15001	Sequence 15001, A
c 21	17	28.3	252	16	US-10-029-386-26242	Sequence 26242, A
c 22	17	28.3	312	17	US-10-282-122A-33901	Sequence 33901, A
c 23	17	28.3	502	20	US-10-357-930-39111	Sequence 39111, A
c 24	17	28.3	502	20	US-10-357-930-44897	Sequence 44897, A
c 25	17	28.3	556	16	US-10-029-386-12542	Sequence 12542, A
c 26	17	28.3	1470	17	US-10-282-122A-33548	Sequence 33548, A
c 27	17	28.3	1809	18	US-10-267-502-97	Sequence 97, Appl
c 28	17	28.3	3048	18	US-10-641-643-957	Sequence 957, App
c 29	17	28.3	256157	13	US-10-087-192-1204	Sequence 1204, Ap
c 30	17	28.3	256157	19	US-10-322-281-776	Sequence 776, App
c 31	16	26.7	542	13	US-10-027-632-283188	Sequence 283188, App
c 32	16	26.7	542	17	US-10-027-632-283188	Sequence 283188, App
c 33	16	26.7	550	17	US-10-388-934-766	Sequence 766, App
c 34	16	26.7	663	18	US-10-404-460-13	Sequence 13, Appl
c 35	16	26.7	1233	13	US-10-027-632-123149	Sequence 123149, App
c 36	16	26.7	1233	17	US-10-027-632-123149	Sequence 123149, App
c 37	16	26.7	1508	19	US-10-437-963-102285	Sequence 102285, App
c 38	16	26.7	1644	16	US-10-060-521-3	Sequence 3, Appli
c 39	16	26.7	1889	10	US-09-532-300-108	Sequence 108, App
c 40	16	26.7	4403	17	US-10-398-221-3755	Sequence 3755, Ap
c 41	16	26.7	4722	19	US-10-437-963-74767	Sequence 74767, A
c 42	16	26.7	8961	17	US-10-062-674-1474	Sequence 1474, Ap
c 43	16	26.7	60327	18	US-10-052-482-187	Sequence 187, App
c 44	16	26.7	77777	19	US-10-318-389-4	Sequence 4, Appli
c 45	16	26.7	79860	13	US-10-087-192-412	Sequence 412, App

ALIGNMENTS

RESULT 1  
US-10-057-136-6  
; Sequence 6, Application US/10057136  
; Publication No. US20030021770A1  
; GENERAL INFORMATION:  
; APPLICANT: SCHLOM, JEFFREY  
; APPLICANT: KANTOR, JUDITH  
; APPLICANT: KUFE, DONALD  
; APPLICANT: PANICALI, DENNIS  
; APPLICANT: GRITZ, LINDA  
; TITLE OF INVENTION: RECOMBINANT POX VIRUS FOR IMMUNIZATION AGAINST MUC1  
; TITLE OF INVENTION: TUMOR-ASSOCIATED ANTIGEN  
; FILE REFERENCE: 700953/47113C  
; CURRENT FILING DATE: 2002-01-25  
; PRIOR APPLICATION NUMBER: 09/366,670  
; PRIOR FILING DATE: 1999-08-03  
; PRIOR APPLICATION NUMBER: PCT/US98/03693  
; PRIOR FILING DATE: 1998-02-24  
; PRIOR APPLICATION NUMBER: 60/038,253  
; PRIOR FILING DATE: 1997-02-24  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 60  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-057-136-6

Query Match 100.0%; Score 60; DB 14; Length 60;

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Best Local Similarity 100.0%; Pred. No. 8.3e-24;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTCAACAGCTCTCCGCTCATGGGTTACTTCTGCTCCAGATCTCGCCAGCTCCA 60
   |||
Db 1 GGGTCAACAGCTCTCCGCTCATGGGTTACTTCTGCTCCAGATCTCGCCAGCTCCA 60
   |||

RESULT 2
US-10-406-317-41
; Sequence 41, Application US/10406317
; Publication No. US20040019195A1
; GENERAL INFORMATION:
; APPLICANT: Schlom, Jeffrey;
; APPLICANT: Hodge, James;
; APPLICANT: Panicali, Dennis
; TITLE OF INVENTION: A recombinant vector expressing multiple constimulatory
; TITLE OF INVENTION: molecules and uses thereof
; FILE REFERENCE: 38163-0189
; CURRENT APPLICATION NUMBER: US/10/406,317
; CURRENT FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: US/09/856,988
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: PCT/US99/26866
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/111,582
; PRIOR FILING DATE: 1998-12-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 2297
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: VECTOR
US-10-406-317-41

Query Match 100.0%; Score 60; DB 17; Length 2297;
Best Local Similarity 100.0%; Pred. No. 6.6e-24;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTCAACAGCTCTCCGCTCATGGGTTACTTCTGCTCCAGATCTCGCCAGCTCCA 60
   |||
Db 526 GGGTCAACAGCTCTCCGCTCATGGGTTACTTCTGCTCCAGATCTCGCCAGCTCCA 585
   |||

RESULT 3
US-10-741-600-3612/c
; Sequence 3612, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3612
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-3612

Query Match 33.3%; Score 20; DB 21; Length 201;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 38 CTCGAGATCTCGCCAGCT 57
   |||
Db 45 CTCGAGATCTCGCCAGCT 26
   |||

RESULT 4
US-10-741-600-3628/c
; Sequence 3628, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3628
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-3628

Query Match 33.3%; Score 20; DB 21; Length 201;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 38 CTCGAGATCTCGCCAGCT 57
   |||
Db 45 CTCGAGATCTCGCCAGCT 26
   |||

RESULT 5
US-10-741-600-3676/c
; Sequence 3676, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3676
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-3676

Query Match 33.3%; Score 20; DB 21; Length 201;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 38 CTCGAGATCTCGCCAGCT 57
   |||
Db 45 CTCGAGATCTCGCCAGCT 26
   |||

RESULT 6
US-09-867-701-1712/c
; Sequence 1712, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Agiate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 1712
; LENGTH: 405
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; LOCATION: (1)-(405)
; OTHER INFORMATION: n = A,T,C or G
US-09-867-701-1712

Query Match      33.3%; Score 20; DB 9; Length 405;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 38 CTCGAGATCTGCGCCAGCT 57
Db 33 CTCGAGATCTGCGCCAGCT 14

RESULT 7
US-10-926-683-517/c
; Sequence 517, Application US/10926683
; Publication No. US20050106595A1
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert A.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: GENSET.025CPI
; CURRENT APPLICATION NUMBER: US/10/926,683
; CURRENT FILING DATE: 2004-08-25
; PRIOR APPLICATION NUMBER: US/09/471,276
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 09/057,719
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 09/069,047
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: PCT/IB99/00712
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 1622
; SOFTWARE: Patent.pm
; SEQ ID NO 517
; LENGTH: 453
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: CDS
; LOCATION: 113..451
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 113..307
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 4.4000009536743
; OTHER INFORMATION: seq FIEALLIHGSAC/VY
US-10-926-683-517

Query Match      33.3%; Score 20; DB 21; Length 453;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 38 CTCGAGATCTGCGCCAGCT 57
Db 217 CTCGAGATCTGCGCCAGCT 198

RESULT 8
US-10-741-600-65/c
; Sequence 65, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001499
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 61
; LENGTH: 2659
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-65

Query Match      33.3%; Score 20; DB 21; Length 2659;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 38 CTCGAGATCTGCGCCAGCT 57
Db 200 CTCGAGATCTGCGCCAGCT 181

RESULT 9
US-10-741-600-62/c
; Sequence 62, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 62
; LENGTH: 2655
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-62

Query Match      33.3%; Score 20; DB 21; Length 2655;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 38 CTCGAGATCTGCGCCAGCT 57
Db 296 CTCGAGATCTGCGCCAGCT 277

RESULT 10
US-10-741-600-61/c
; Sequence 61, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 61
; LENGTH: 2659
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-61

Query Match      33.3%; Score 20; DB 21; Length 2659;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 38 CTCGAGATCTGCGCCAGCT 57
Db 200 CTCGAGATCTGCGCCAGCT 181
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Db      296 CTCGAGATACGCGCCAGCT 277

RESULT 11
US-10-741-600-17923
; Sequence 17923, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17923
; LENGTH: 16747
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-17923

Query Match      33.3%; Score 20; DB 21; Length 16747;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      38 CTCGAGATACGCGCCAGCT 57
|||||
Db      5253 CTCGAGATACGCGCCAGCT 5272

RESULT 12
US-10-741-600-17578/c
; Sequence 17578, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17578
; LENGTH: 27875
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(27875)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-741-600-17578

Query Match      33.3%; Score 20; DB 21; Length 27875;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      38 CTCGAGATACGCGCCAGCT 57
|||||
Db      6295 CTCGAGATACGCGCCAGCT 6276

RESULT 13
US-10-437-963-97051/c
; Sequence 97051, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 97051
; LENGTH: 1228
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_95091C.1
US-10-437-963-97051

Query Match      30.0%; Score 18; DB 19; Length 1228;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      31 ACTTCTGCTCCAGATACT 48
|||||
Db      720 ACTTCTGCTCCAGATACT 703

RESULT 14
US-10-437-963-97047/c
; Sequence 97047, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 97047
; LENGTH: 2493
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_95088C.1
US-10-437-963-97047

Query Match      30.0%; Score 18; DB 19; Length 2493;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      31 ACTTCTGCTCCAGATACT 48
|||||
Db      2416 ACTTCTGCTCCAGATACT 2399

RESULT 15
US-09-735-367B-5
; Sequence 5, Application US/09735367B
; Patent No. US20020151477A1
; GENERAL INFORMATION:
; APPLICANT: Gustafsson, Jan-Ake
; APPLICANT: Cairra, Francoise
; APPLICANT: Antonsson, Per
; TITLE OF INVENTION: NUCLEAR RECEPTOR COACTIVATOR
; FILE REFERENCE: 102093-100
; CURRENT APPLICATION NUMBER: US/09/735,367B
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; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: US 60/174,544
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 3899
; TYPE: DNA
; ORGANISM: mammal
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (203)...(3415)
US-09-735-367B-5
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Query Match      30.0%; Score 18; DB 9; Length 3899;
Best Local Similarity 100.0%; Pred.No. 3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      40 CCAGATACCTCGCCGAGCT 57
          |||||
Db      2999 CCAGATACCTCGCCGAGCT 3016
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Search completed: June 30, 2005, 04:44:46
Job time : 358.7 secs
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 29, 2005, 19:26:35 ; Search time 51.2 Seconds  
(without alignments)  
1917.512 Million cell updates/sec

**Title:** US-10-057-136-6

Perfect score: 60

Sequence: 1 ggggtcaacagctcctccgc.....cagatactcgccagctcca 60

Scoring table: **OLIGO\_NUC**  
Gapop 60.0 , Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents N

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2: /cgm2_6/pdata1/ina/5B_COMB.seq.*
3: /cgm2_6/pdata1/ina/6A_COMB.seq.*
4: /cgm2_6/pdata1/ina/6B_COMB.seq.*
5: /cgm2_6/pdata1/ina/PCTUS_COMB.seq.*
6: /cgm2_6/pdata1/ina/backfiles1.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	20	33.3	453	4	US-09-471-276-517	Sequence 517, App
C 2	20	33.3	511	4	US-09-621-976-1594	Sequence 1594, App
C 3	17	28.3	3048	4	US-09-023-655-957	Sequence 957, App
C 4	17	28.3	240157	4	US-09-949-016-16264	Sequence 16264, A
C 5	16	26.7	1512	4	US-09-270-767-15148	Sequence 15148, A
C 6	16	26.7	27617	4	US-09-949-016-17040	Sequence 17040, A
C 7	16	26.7	246444	4	US-09-949-016-13113	Sequence 13113, A
C 8	15	25.0	30	1	US-08-410-739-1	Sequence 1, Appli
C 9	15	25.0	30	1	US-08-697-815-1	Sequence 1, Appli
C 10	15	25.0	30	2	US-09-061-286-1	Sequence 1, Appli
C 11	15	25.0	327	4	US-09-313-294A-7059	Sequence 7059, App
C 12	15	25.0	375	4	US-09-513-999C-13614	Sequence 13614, A
C 13	15	25.0	415	4	US-09-270-767-30904	Sequence 30904, A
C 14	15	25.0	417	4	US-09-513-999C-10290	Sequence 10290, A
C 15	15	25.0	488	4	US-09-513-999C-10293	Sequence 10293, A
C 16	15	25.0	601	4	US-09-949-016-39033	Sequence 39033, A
C 17	15	25.0	601	4	US-09-949-016-142149	Sequence 142149, App
C 18	15	25.0	601	4	US-09-949-016-158466	Sequence 158466, App
C 19	15	25.0	601	4	US-09-949-016-158467	Sequence 158467, App
C 20	15	25.0	601	4	US-09-949-016-158468	Sequence 158468, App
C 21	15	25.0	601	4	US-09-949-016-178512	Sequence 178512, App
C 22	15	25.0	822	4	US-09-023-655-1078	Sequence 1078, App
C 23	15	25.0	874	4	US-09-513-999C-14943	Sequence 14943, A
C 24	15	25.0	888	4	US-09-949-016-4424	Sequence 4424, App
C 25	15	25.0	947	4	US-09-919-039-332	Sequence 332, App
C 26	15	25.0	1186	4	US-09-513-999C-14929	Sequence 14929, A
C 27	15	25.0	1325	4	US-09-566-921-131	Sequence 131, App

C 28	15	25.0	1629	3	US-08-939-309-5	Sequence 5, Appli
C 29	15	25.0	1629	4	US-09-849-180-5	Sequence 5, Appli
C 30	15	25.0	1629	4	US-09-358-643B-3	Sequence 3, Appli
C 31	15	25.0	1629	4	US-10-053-510-3	Sequence 3, Appli
C 32	15	25.0	1827	4	US-09-603-787A-29	Sequence 29, Appli
C 33	15	25.0	2212	4	US-09-270-767-14682	Sequence 29, Appli
C 34	15	25.0	2697	4	US-09-949-016-5116	Sequence 14682, A
C 35	15	25.0	3401	4	US-09-907-794A-249	Sequence 249, App
C 36	15	25.0	3401	4	US-09-905-125A-249	Sequence 249, App
C 37	15	25.0	3401	4	US-09-902-775A-249	Sequence 249, App
C 38	15	25.0	3401	4	US-09-905-700-249	Sequence 249, App
C 39	15	25.0	3401	4	US-09-903-603A-249	Sequence 249, App
C 40	15	25.0	3401	4	US-09-904-920A-249	Sequence 249, App
C 41	15	25.0	3401	4	US-09-909-064-249	Sequence 249, App
C 42	15	25.0	3401	4	US-09-905-381A-249	Sequence 249, App
C 43	15	25.0	3401	4	US-09-906-618-249	Sequence 249, App
C 44	15	25.0	3747	2	US-09-080-897-1	Sequence 1, Appli
C 45	15	25.0	3747	3	US-09-323-735-1	Sequence 1, Appli

## ALIGNMENTS

```

RESULT 1
US-09-471-276-517/c
; Sequence 517, Application US/09471276
; Patent No. 6822072
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6822072
; FILE REFERENCE: GENSET-025CP1
; CURRENT APPLICATION NUMBER: US/09/471,276
; CURRENT FILING DATE: 1999-12-21
; EARLIER APPLICATION NUMBER: 09/057,719
; EARLIER FILING DATE: 1998-04-09
; EARLIER APPLICATION NUMBER: 09/069,047
; EARLIER FILING DATE: 1998-04-28
; EARLIER APPLICATION NUMBER: PCT/IB99/00712
; EARLIER FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 1622
; SOFTWARE: Patent.pm
; SEQ ID NO 517
; LENGTH: 453
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 113..451
; NAME/KEY: sig_peptide
; LOCATION: 113..307
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 4.40000009536743
; OTHER INFORMATION: seg FIEAALLHGSAC/VY
US-09-471-276-517

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Query Match	33.3%;	Score 20;	DB 4;	Length 453;
Best Local Similarity	100.0%;	Pred. No. 0.48;		
Matches 20;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	38	CTCCAGATACTGCCCCAGCT	57	
Db	217	CTCCAGATACTGCCCCAGCT	198	

RESULT 2  
US-09-621-976-1594/c  
; Sequence 1594, Application US/09621976  
; Patent No. 6639083  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.

; APPLICANT: Jobert, S.  
; APPLICANT: Giordano, J.V.  
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
; FILE REFERENCE: GENSET.054PR2  
; CURRENT APPLICATION NUMBER: US/09/621,976  
; CURRENT FILING DATE: 2000-07-21  
; NUMBER OF SEQ ID NOS: 19335  
; SOFTWARE: Patent.pm  
; SEQ ID NO 1594  
; LENGTH: 511  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 99..443  
; NAME/KEY: sig\_peptide  
; LOCATION: 99..293  
; OTHER INFORMATION: Von Heijne matrix  
; . OTHER INFORMATION: score 5.9000009536743  
; . OTHER INFORMATION: seq FIEAALLIQSAA/ST  
US-09-621-976-1594

Query Match 33.3%; Score 20; DB 4; Length 511;  
Best Local Similarity 100.0%; Pred. No. 0.48;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 38 CTCGAGATCTCGCCGAGCT 57  
Db 203 CTCGAGATCTCGCCGAGCT 184

RESULT 3  
US-09-023-655-957/c  
; Sequence 957, Application US/09023655  
; Patent No. 6607879  
; GENERAL INFORMATION:  
; APPLICANT: Cocks, Benjamin G.  
; APPLICANT: Susan G. Stuart  
; APPLICANT: Jeffrey J. Seilhamer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE  
; TITLE OF INVENTION: EXPRESSION  
; NUMBER OF SEQUENCES: 1508  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/023,655  
; FILING DATE: HERewith  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Zeller, Karen J.  
; REGISTRATION NUMBER: 37,071  
; REFERENCE/DOCKET NUMBER: PA-0001 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 855-0555  
; TELEFAX: (650) 845-4166  
; INFORMATION FOR SEQ ID NO: 957:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3048 base pairs  
; TYPE: nucleic acid

; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: GENBANK  
; CLONE: g1478067  
US-09-023-655-957

Query Match 28.3%; Score 17; DB 4; Length 3048;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 AACAGCTCTCCCGCTC 22  
Db 540 AACAGCTCTCCCGCTC 524

## RESULT 4

US-09-949-016-16264  
; Sequence 16264, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 16264  
; LENGTH: 240157  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(240157)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-16264

Query Match 28.3%; Score 17; DB 4; Length 240157;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 31 ACTTCTGCTCCAGATAC 47  
Db 104643 ACTTCTGCTCCAGATAC 104659

## RESULT 5

US-09-270-767-15148/c  
; Sequence 15148, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 15148  
; LENGTH: 1512  
; TYPE: DNA  
; ORGANISM: Drosophila melanogaster  
US-09-270-767-15148

Query Match 26.7%; Score 16; DB 4; Length 1512;



Best Local Similarity 100.0%; Pred. No. 55;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 AACAGCTCTCCCGCT 21  
|||||  
Db 611 AACAGCTCTCCCGCT 596

RESULT 6  
US-09-949-016-17040/c  
; Sequence 17040, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CLO01307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 17040  
; LENGTH: 27617  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-17040

Query Match 26.7%; Score 16; DB 4; Length 27617;  
Best Local Similarity 100.0%; Pred. No. 56;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 CTTCTGCTCCAGATAC 47  
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Db 2810 CTTCTGCTCCAGATAC 2795

RESULT 7  
US-09-949-016-13113/c  
; Sequence 13113, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CLO01307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13113  
; LENGTH: 246444  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)...(246444)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-13113

Query Match 26.7%; Score 16; DB 4; Length 246444;  
Best Local Similarity 100.0%; Pred. No. 57;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 30 TACTTCTGCTCCAGAT 45  
|||||  
Db 193625 TACTTCTGCTCCAGAT 193610

RESULT 8  
US-08-410-739-1/c  
; Sequence 1, Application US/08410739  
; Patent No. 5759836  
; GENERAL INFORMATION:  
; APPLICANT: AMIN, Ashok R.  
; APPLICANT: ABRAMSON, Steven B.  
; TITLE OF INVENTION: A NOVEL NITRIC OXIDE SYNTHASE,  
; TITLE OF INVENTION: ANTIBODIES THERETO AND METHOD OF SCREENING COMPOUNDS FOR  
; TITLE OF INVENTION: INHIBITION OF SAME  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA: US/08/410,739  
; APPLICATION NUMBER: US/08/410,739  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: YUN, Allen C.  
; REGISTRATION NUMBER: 37,971  
; REFERENCE/DOCKET NUMBER: AMIN=1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; TELEX: 248633  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 30 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
US-08-410-739-1

Query Match 25.0%; Score 15; DB 1; Length 30;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 31 ACTTCTGCTCCAGAT 45  
|||||  
Db 29 ACTTCTGCTCCAGAT 15

RESULT 9  
US-08-697-815-1/c  
; Sequence 1, Application US/08697815  
; Patent No. 5789395  
; GENERAL INFORMATION:  
; APPLICANT: Amin, Ashok R  
; APPLICANT: Abramson, Steven B  
; APPLICANT: Golub, Lorne M  
; APPLICANT: Ramamurthy, Nungavaram S  
; APPLICANT: McNamara, Thomas P  
; APPLICANT: Greenwald, Robert  
; APPLICANT: Trachtman, Howard  
; TITLE OF INVENTION: Method of Using Tetracycline Compounds

;; TITLE OF INVENTION: for Inhibition of Nitric Oxide Production  
;; NUMBER OF SEQUENCES: 4  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: HOFFMANN & BARON  
;; STREET: 350 Jericho Turnpike  
;; CITY: Jericho  
;; STATE: New York  
;; COUNTRY: USA  
;; ZIP: 11753  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patentin Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA: US/08/697,815  
;; FILING DATE:  
;; CLASSIFICATION:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: O'Dea, Sean W  
;; REGISTRATION NUMBER: 37,690  
;; REFERENCE/DOCKET NUMBER: 178-218  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (516) 822-3550  
;; TELEFAX: (516) 822-3582  
;; INFORMATION FOR SEQ ID NO: 1:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 30 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: other nucleic acid  
;; HYPOTHETICAL: NO  
;; ANTI-SENSE: NO  
;; US-08-697-815-1

Query Match 25.0%; Score 15; DB 1; Length 30;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 31 ACTTCTGCTCCAGAT 45  
Db 29 ACTTCTGCTCCAGAT 15

## RESULT 10

US-09-061-286-1/c  
; Sequence 1, Application US/09061286  
; Patent No. 5919775

## GENERAL INFORMATION:

;; APPLICANT: Amin, Ashok R  
;; APPLICANT: Abramson, Steven B  
;; APPLICANT: Golub, Lorne M  
;; APPLICANT: Ramamurthy, Nungavaram S  
;; APPLICANT: McNamara, Thomas F  
;; APPLICANT: Greenwald, Robert  
;; APPLICANT: Trachtman, Howard  
;; TITLE OF INVENTION: Method of Using Tetracycline  
;; TITLE OF INVENTION: Compounds For Inhibition of Nitric Oxide Production  
;; NUMBER OF SEQUENCES: 4  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: HOFFMANN & BARON, LLP  
;; STREET: 350 Jericho Turnpike  
;; CITY: Jericho  
;; STATE: New York  
;; COUNTRY: USA  
;; ZIP: 11753

## COMPUTER READABLE FORM:

;; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Wordperfect  
;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/09/061,286  
;; FILING DATE:  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/697,815  
;; FILING DATE: 30-AUGUST-1996  
;; CLASSIFICATION:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: O'Dea, Sean W.  
;; REGISTRATION NUMBER: 37690  
;; REFERENCE/DOCKET NUMBER: 178-218 DIV  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (516) 822-3550  
;; TELEFAX: (516) 822-3582  
;; INFORMATION FOR SEQ ID NO: 1:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 30 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: other nucleic acid  
;; HYPOTHETICAL: NO  
;; ANTI-SENSE: NO  
;; US-09-061-286-1

Query Match 25.0%; Score 15; DB 2; Length 30;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 31 ACTTCTGCTCCAGAT 45  
Db 29 ACTTCTGCTCCAGAT 15

## RESULT 11

US-09-313-294A-7059/c  
; Sequence 7059, Application US/09313294A  
; Patent No. 6476212

## GENERAL INFORMATION:

;; APPLICANT: Lalgudi, Raghunath V.  
;; APPLICANT: Ito, Laura Y.  
;; APPLICANT: Sherman, Bradley K.  
;; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR  
;; FILE REFERENCE: PL-0017 US  
;; CURRENT APPLICATION NUMBER: US/09/313,294A  
;; CURRENT FILING DATE: 1999-05-14  
;; NUMBER OF SEQ ID NOS: 7600  
;; SOFTWARE: PERL Program  
;; SEQ ID NO 7059  
;; LENGTH: 327  
;; TYPE: DNA  
;; ORGANISM: Zea mays  
;; FEATURE:  
;; NAME/KEY: misc feature  
;; OTHER INFORMATION: Incyte ID No. 6476212 700381058H1  
;; NAME/KEY: unsure  
;; LOCATION: 28, 162, 275  
;; OTHER INFORMATION: a, t, c, g, or other  
;; US-09-313-294A-7059

Query Match 25.0%; Score 15; DB 4; Length 327;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 42 AGATACCTCGCCAGC 56  
Db 271 AGATACCTCGCCAGC 257

## RESULT 12

US-09-513-999C-13614/c  
; Sequence 13614, Application US/09513999C  
; Patent No. 6783961

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; LENGTH: 417
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 6
; OTHER INFORMATION: n=a, g, c or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 200
; OTHER INFORMATION: m=a or c
US-09-513-999C-10290

Query Match      25.0%; Score 15; DB 4; Length 417;
Best Local Similarity 100.0%; Pred.No.1.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      42 AGATACTCGCCCGCAGC 56
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Db      271 AGATACTCGCCCGCAGC 257

RESULT 15
US-09-513-999C-10293/c
; Sequence 10293, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 10293
; LENGTH: 488
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 6
; OTHER INFORMATION: n=a, g, c or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 271
; OTHER INFORMATION: m=a or c
US-09-513-999C-10293

Query Match      25.0%; Score 15; DB 4; Length 488;
Best Local Similarity 100.0%; Pred.No.1.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      42 AGATACTCGCCCGCAGC 56
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Db      342 AGATACTCGCCCGCAGC 328

Search completed: June 30, 2005, 04:04:22
Job time : 90.2 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 29, 2005, 23:23:45 ; Search time 230.7 Seconds  
(without alignments)  
1625.622 Million cell updates/sec

Title: US-10-057-136-7

Perfect score: 60

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Searched: 6067389 seqs, 3125258755 residues

Word size : 0

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Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

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- 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*
- 12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*
- 13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*
- 14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*
- 15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*
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- 17: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq:\*
- 18: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq:\*
- 19: /cgn2\_6/ptodata/1/pubpna/US10G\_PUBCOMB.seq:\*
- 20: /cgn2\_6/ptodata/1/pubpna/US10H\_PUBCOMB.seq:\*
- 21: /cgn2\_6/ptodata/1/pubpna/US10I\_PUBCOMB.seq:\*
- 22: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*
- 23: /cgn2\_6/ptodata/1/pubpna/US11A\_PUBCOMB.seq:\*
- 24: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq:\*
- 25: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*
- 26: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	60	100.0	2297	17	US-10-406-317-41
3	17	28.3	867	17	US-10-369-493-33682
4	17	28.3	1171	20	US-10-425-115-66540
5	16	26.7	406	10	US-09-918-995-36727
6	16	26.7	465	10	US-09-918-995-32117
7	16	26.7	769	20	US-10-425-115-92232

Sequence 7, Appli

Sequence 41, Appl

Sequence 33682, A

Sequence 66540, A

Sequence 36727, A

Sequence 32117, A

Sequence 92232, A

Query Match

100.0%; Score 60; DB 14; Length 60;

Sequence 1517, Ap

Sequence 38104, A

Sequence 35087, A

Sequence 38514, A

Sequence 38696, A

Sequence 143, App

Sequence 812, App

Sequence 813, App

Sequence 9103, Ap

Sequence 9104, Ap

Sequence 788, App

Sequence 16, Appl

Sequence 34287, A

Sequence 36307, A

Sequence 23480, A

Sequence 2843, Ap

Sequence 174502, A

Sequence 74836, A

Sequence 33184, A

Sequence 42109, A

Sequence 5648, Ap

Sequence 21830, A

Sequence 27677, A

Sequence 29386, A

Sequence 29387, A

Sequence 21091, A

Sequence 134229, A

Sequence 134230, A

Sequence 134230, A

Sequence 12012, A

Sequence 179856, A

Sequence 1799, Ap

Sequence 14257, A

Sequence 13, Appl

#### ALIGNMENTS

#### RESULT 1

US-10-057-136-7

; Sequence 7, Application US/10057136

; Publication No. US20030021770A1

; GENERAL INFORMATION: SCHLOM, JEFFREY

; APPLICANT: KANTOR, JUDITH

; APPLICANT: KUFE, DONALD

; APPLICANT: PANICALI, DENNIS

; APPLICANT: GRITZ, LINDA

; TITLE OF INVENTION: RECOMBINANT POX VIRUS FOR IMMUNIZATION AGAINST MUC1

; TITLE OF INVENTION: TUMOR-ASSOCIATED ANTIGEN

; FILE REFERENCE: 700953/47113C

; CURRENT APPLICATION NUMBER: US/10/057,136

; PRIOR FILING DATE: 2002-01-25

; PRIOR APPLICATION NUMBER: 09/366,670

; PRIOR FILING DATE: 1999-08-03

; PRIOR APPLICATION NUMBER: PCT/US98/03693

; PRIOR FILING DATE: 1998-02-24

; PRIOR APPLICATION NUMBER: 60/038,253

; PRIOR FILING DATE: 1997-02-24

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 7

; LENGTH: 60

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-057-136-7

Best Local Similarity 100.0%; Pred. No. 7.3e-25;  
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGTTCGACGGCCCCCTGCTCAGGGTGAACATCCGGCCCGGATACAGACCGGCCCT 60  
Db 1 GGTTCGACGGCCCCCTGCTCAGGGTGAACATCCGGCCCGGATACAGACCGGCCCT 60

RESULT 2  
US-10-406-317-41  
; Sequence 41, Application US/10406317  
; Publication No. US20040019195A1  
; GENERAL INFORMATION:  
; APPLICANT: Schlom, Jeffrey;  
; APPLICANT: Hodge, James;  
; APPLICANT: Panicali, Dennis  
; TITLE OF INVENTION: A recombinant vector expressing multiple constimulatory  
; TITLE OF INVENTION: molecules and uses thereof  
; FILE REFERENCE: 38163-0189  
; CURRENT APPLICATION NUMBER: US/10/406,317  
; CURRENT FILING DATE: 2003-04-04  
; PRIOR APPLICATION NUMBER: US/09/856,988  
; PRIOR FILING DATE: 2001-05-30  
; PRIOR APPLICATION NUMBER: PCT/US99/26866  
; PRIOR FILING DATE: 1999-11-12  
; PRIOR APPLICATION NUMBER: 60/111,582  
; PRIOR FILING DATE: 1998-12-09  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 41  
; LENGTH: 2297  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: VECTOR  
US-10-406-317-41

Query Match 100.0%; Score 60; DB 17; Length 2297;  
Best Local Similarity 100.0%; Pred. No. 4.5e-25;  
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGTTCGACGGCCCCCTGCTCAGGGTGAACATCCGGCCCGGATACAGACCGGCCCT 60  
Db 586 GGTTCGACGGCCCCCTGCTCAGGGTGAACATCCGGCCCGGATACAGACCGGCCCT 645

RESULT 3  
US-10-369-493-33682  
; Sequence 33682, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10/369,493  
; CURRENT FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 33682  
; LENGTH: 867  
; TYPE: DNA  
; ORGANISM: magnetite-containing magnetic coccus  
US-10-369-493-33682  
Query Match 28.3%; Score 17; DB 17; Length 867;  
Best Local Similarity 100.0%; Pred. No. 5.4;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGTTCGACGGCCCCCTGCTCAGGGTGAACATCCGGCCCGGATACAGACCGGCCCT 17  
Db 706 GGTTCGACGGCCCCCTGCTCAGGGTGAACATCCGGCCCGGATACAGACCGGCCCT 722

RESULT 4  
US-10-425-115-66540/c  
; Sequence 66540, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 66540  
; LENGTH: 1171  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_160683C.1  
US-10-425-115-66540

Query Match 28.3%; Score 17; DB 20; Length 1171;  
Best Local Similarity 100.0%; Pred. No. 5.2;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 14 CCCTGCTCAGGTGTA 30  
Db 1048 CCCTGCTCAGGTGTA 1032

RESULT 5  
US-09-918-995-36727/c  
; Sequence 36727, Application US/09918995  
; Publication No. US20030073623A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES  
; FILE REFERENCE: 20411-756  
; CURRENT APPLICATION NUMBER: US/09/918,995  
; CURRENT FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: US/09/235,076  
; PRIOR FILING DATE: 1999-01-20  
; NUMBER OF SEQ ID NOS: 38054  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 36727  
; LENGTH: 406  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-918-995-36727

Query Match 26.7%; Score 16; DB 10; Length 406;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 9 GGCCCCCTGCTCAC 24  
Db 226 GGCCCCCTGCTCAC 211

RESULT 6  
US-09-918-995-32117/c  
; Sequence 32117, Application US/09918995  
; Publication No. US20030073623A1

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Query Match      26.7%; Score 16; DB 15; Length 1153;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 16: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 13 CCCCTGCTCAGGTG 28  
Db 162 CCCCTGCTCAGGTG 147

RESULT 9  
US-10-369-493-38104/c

RESULT 9  
 US-10-369-493-38104/c  
 ; Sequence 38104, Application US/10369493  
 ; Publication No. US2003023675A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cao, Yongwei  
 ; APPLICANT: Hinkle, Gregory J.  
 ; APPLICANT: Slater, Steven C.  
 ; APPLICANT: Goldman, Barry S.  
 ; APPLICANT: Chen, Xianfeng  
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
 ; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES  
 ; FILE REFERENCE: 38-10(52052)B  
 ; CURRENT APPLICATION NUMBER: US/10/369,493  
 ; CURRENT FILING DATE: 2003-02-28  
 ; PRIOR APPLICATION NUMBER: US 60/360,039  
 ; PRIOR FILING DATE: 2002-02-21  
 ; NUMBER OF SEQ ID NOS: 47374  
 ; SEQ ID NO 38104  
 ; LENGTH: 1194  
 ; TYPE: DNA  
 ; ORGANISM: Agrobacterium tumefaciens  
 ; US-10-369-493-38104

Query Match 26.7%; Score 16; DB 17; Length 1194;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 16; Conservative 0; Mismatches 0; Indels

Qy 45 TACCAGACGGCCCT 60  
Db 833 TACCAGACGGCCCT 818

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RESULT 10
US-10-369-493-35087/c
; Sequence 35087, Application US/10369493
; Publication No. US2003023675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICRO
; TITLE OF INVENTION: PLANTS WITH IMPRO
; FILE REFERENCE: 38-10 (52052)B
; CURRENT APPLICATION NUMBER: US/10/369,

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RESULT 12  
US-10-369-493-38696/c  
; Sequence 38696, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkie, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10/369,493  
; CURRENT FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 38696  
; LENGTH: 2088  
; TYPE: DNA

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RESULT 14
US-09-764-872-812/c
; Sequence 812, Application US/09764872
; Publication No. US20030050231A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA125
; CURRENT APPLICATION NUMBER: US/09/764,872
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 957
; SOFTWARE: Patent In Ver. 2.0

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

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(without alignments)  
1917.512 Million cell updates/sec

Title: US-10-057-136-7

Perfect score: 60

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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C 4	15	25.0	312	4	US-09-513-999C-13405
C 5	15	25.0	548	4	US-09-621-976-2414
C 6	15	25.0	2202	4	US-09-489-039A-5397
C 7	15	25.0	2975	1	US-08-368-281-1
C 8	15	25.0	7305	4	US-09-902-540-961
C 9	15	25.0	11958	3	US-09-134-246-8
C 10	15	25.0	11958	4	US-09-664-186-8
C 11	15	25.0	36618	4	US-09-949-016-16935
C 12	15	25.0	118067	4	US-09-497-855A-32
C 13	14	23.3	34	2	US-08-930-274-3
C 14	14	23.3	83	2	US-08-894-228-9
C 15	14	23.3	83	3	US-09-191-521-9
C 16	14	23.3	83	3	US-09-133-321-10
C 17	14	23.3	84	4	US-09-513-999C-16843
C 18	14	23.3	401	4	US-09-621-976-13452
C 19	14	23.3	428	4	US-09-902-540-9336
C 20	14	23.3	521	3	US-09-404-879A-115
C 21	14	23.3	521	4	US-09-338-933-115
C 22	14	23.3	521	4	US-09-215-681-115
C 23	14	23.3	521	4	US-09-216-003A-115
C 24	14	23.3	521	4	US-09-667-857-115
C 25	14	23.3	601	4	US-09-949-016-44522
C 26	14	23.3	601	4	US-09-949-016-44523
C 27	14	23.3	601	4	US-09-949-016-49677

C 28	14	23.3	601	4	US-09-949-016-49678	Sequence 49678, A
C 29	14	23.3	601	4	US-09-949-016-49679	Sequence 49679, A
C 30	14	23.3	601	4	US-09-949-016-49680	Sequence 49680, A
C 31	14	23.3	601	4	US-09-949-016-63347	Sequence 63347, A
C 32	14	23.3	701	3	US-09-133-321-1	Sequence 1, Appli
C 33	14	23.3	768	3	US-09-328-111-667	Sequence 667, App
C 34	14	23.3	831	4	US-09-902-540-5839	Sequence 5839, Ap
C 35	14	23.3	867	4	US-09-902-540-7166	Sequence 7166, Ap
C 36	14	23.3	894	1	US-08-076-726-10	Sequence 10, Appli
C 37	14	23.3	894	1	US-08-260-452-3	Sequence 3, Appli
C 38	14	23.3	894	2	US-08-481-970-3	Sequence 3, Appli
C 39	14	23.3	894	2	US-08-897-719-3	Sequence 3, Appli
C 40	14	23.3	894	3	US-09-163-269-3	Sequence 3, Appli
C 41	14	23.3	894	4	US-09-281-674-3	Sequence 3, Appli
C 42	14	23.3	932	1	US-08-458-912-1	Sequence 1, Appli
C 43	14	23.3	932	1	US-08-461-179-1	Sequence 1, Appli
C 44	14	23.3	932	1	US-08-459-254-1	Sequence 1, Appli
C 45	14	23.3	932	1	US-08-459-255-1	Sequence 1, Appli

## ALIGNMENTS

RESULT 1  
US-08-822-586-45/c  
; Sequence 45, Application US/08822586  
; Patent No. 6015890  
; GENERAL INFORMATION:  
; APPLICANT: WILLIAM R. JACOBS, JR., JAMES M. MUSSER AND  
; APPLICANT: AMALIO TELENTO  
; TITLE OF INVENTION: AN EMBEDED OPERON OF MYCOBACTERIA AND  
; TITLE OF INVENTION: MUTANTS THEREOF  
; NUMBER OF SEQUENCES: 57  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: AMSTER, ROTHSTEIN & EBENSTEIN  
; STREET: 90 PARK AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: U.S.A.  
; ZIP: 10016  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 INCH 1.44 Mb STORAGE  
; MEDIUM TYPE: DISKETTE  
; COMPUTER: IBM PC COMPATIBLE  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/822,586  
; FILING DATE: MARCH 20, 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: ELIZABETH A. BOGOSIAN  
; REGISTRATION NUMBER: 39,911  
; REFERENCE/DOCKET NUMBER: 96700/437  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 697-5995  
; TELEFAX: (212) 286-0854 or 286-0082  
; TELEX: TWX 710-581-4766  
; INFORMATION FOR SEQ ID NO: 45:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10095  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: Genomic DNA  
; HYPOTHETICAL: NO  
US-08-822-586-45

Query Match 26.7%; Score 16; DB 3; Length 10095;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

36 CGCCCGGATACAGCA 51

|||||

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Db 3718 CGCCCCGGATACCAGA 3703

RESULT 2
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match 26.7%; Score 16; DB 3; Length 4403765;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 36 CGCCCCGGATACCAGA 51
|||||

Db 4235673 CGCCCCGGATACCAGA 4235658

RESULT 3
US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match 26.7%; Score 16; DB 3; Length 4411529;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 36 CGCCCCGGATACCAGA 51
|||||

Db 4243427 CGCCCCGGATACCAGA 4243412

RESULT 4
US-09-513-999C-13405
; Sequence 13405, Application US/09513999C

; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 13405
; LENGTH: 312
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 132
; OTHER INFORMATION: m=a or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 143
; OTHER INFORMATION: m=a or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 145
; OTHER INFORMATION: y=c or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 147
; OTHER INFORMATION: s=g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 309
; OTHER INFORMATION: y=c or t
US-09-513-999C-13405

Query Match 25.0%; Score 15; DB 4; Length 312;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 ACGCCCCCTGCT 21
|||||
Db 87 ACGCCCCCTGCT 101

RESULT 5
US-09-621-976-2414
; Sequence 2414, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 2414
; LENGTH: 548
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 95...376
US-09-621-976-2414

Query Match 25.0%; Score 15; DB 4; Length 548;
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Best Local Similarity 100.0%; Pred. No. 49;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 ACGGCCCTGCT 21
Db 113 ACGGCCCTGCT 127

RESULT 6
US-09-489-039A-5397/c
; Sequence 5397, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 5397
; LENGTH: 2202
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
; US-09-489-039A-5397

Query Match 25.0%; Score 15; DB 4; Length 2202;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 40 CCGATACGACCG 54
Db 1592 CCGATACGACCG 1578

RESULT 7
US-08-368-281-1
; Sequence 1, Application US/08368281
; Patent No. 5721113
; GENERAL INFORMATION:
; APPLICANT: Libermann, Towia A
; APPLICANT: Oettgen, Joerg P
; APPLICANT: Kunsch, Charles A
; TITLE OF INVENTION: NERF Genes
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Smithkline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/368,281
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Baumeister, Kirk
; REGISTRATION NUMBER: 33,833
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5096
; TELEFAX: 610-270-5090
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2975 base pairs
; TYPE: nucleic acid
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; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-368-281-1

Query Match 25.0%; Score 15; DB 1; Length 2975;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 CTGCTCAGGTGTA 31
Db 70 CTGCTCAGGTGTA 84

RESULT 8
US-09-902-540-961
; Sequence 961, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 961
; LENGTH: 7305
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; US-09-902-540-961

Query Match 25.0%; Score 15; DB 4; Length 7305;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 34 TCCGCCCGGATACC 48
Db 4255 TCCGCCCGGATACC 4269

RESULT 9
US-09-134-246-8
; Sequence 8, Application US/09134246B
; Patent No. 6207377
; GENERAL INFORMATION:
; APPLICANT: Wayne, Jay
; APPLICANT: Xu, Shuang-yong
; TITLE OF INVENTION: Method For Construction Of Thermus-E. coli Shuttle
; TITLE OF INVENTION: Vectors And Identification Of Two Thermus Plasmid
; TITLE OF INVENTION: Replication Origins
; FILE REFERENCE: Thermus Shuttle Vector
; CURRENT APPLICATION NUMBER: US/09/134,246B
; CURRENT FILING DATE: 1998-08-14
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 11958
; TYPE: DNA
; ORGANISM: Thermus sp.
; US-09-134-246-8

Query Match 25.0%; Score 15; DB 3; Length 11958;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 CCCCCCTGCTACCG 26
Db 11709 CCCCCCTGCTACCG 11723
```

APPLICANT: Huang, Tim	APPLICANT: Wayne, Jay	APPLICANT: Xu, Shuang-yong	APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR DETECTING DNA METHYLATION	TITLE OF INVENTION: Method For Construction Of Thermus-E. coli Shuttle Vectors And Identification Of Two Thermus Plasmid	TITLE OF INVENTION: Polymorphisms In Known Genes Associated With Human Disease, Methods Of Detection And Uses Thereof	TITLE OF INVENTION: Polymorphisms In Known Genes Associated With Human Disease, Methods Of Detection And Uses Thereof
FILE REFERENCE: UMO1523	FILE REFERENCE: US/09664186	FILE REFERENCE: US/09949016	FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: 2000-02-04	CURRENT APPLICATION NUMBER: 2000-09-18	CURRENT APPLICATION NUMBER: 2000-04-14	CURRENT APPLICATION NUMBER: 2000-04-14
PRIOR FILING DATE: 1999-02-18	PRIOR FILING DATE: 2000-09-18	PRIOR FILING DATE: 2000-10-20	PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/120,592	PRIOR APPLICATION NUMBER: 60/134,246B	PRIOR APPLICATION NUMBER: 60/237,768	PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 1999-02-05	PRIOR FILING DATE: 1998-08-14	PRIOR FILING DATE: 2000-10-03	PRIOR FILING DATE: 2000-10-03
NUMBER OF SEQ ID NOS: 54	NUMBER OF SEQ ID NOS: 30	NUMBER OF SEQ ID NOS: 207012	NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PatentIn version 3.0	SOFTWARE: PatentIn Ver. 2.0	SOFTWARE: FastSeq for Windows Version 4.0	SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 32	SEQ ID NO 8	SEQ ID NO 16935	SEQ ID NO 16935
LENGTH: 118067	LENGTH: 11958	LENGTH: 36618	LENGTH: 36618
TYPE: DNA	TYPE: DNA	TYPE: DNA	TYPE: DNA
ORGANISM: Homo sapiens;	ORGANISM: Thermus sp.	ORGANISM: Human	ORGANISM: Human
US-09-497-855A-32	US-09-664-186-8	US-09-949-016-16935	US-09-949-016-16935
Query Match 25.0%; Score 15; DB 4; Length 118067;	Query Match 25.0%; Score 15; DB 4; Length 11958;	Query Match 25.0%; Score 15; DB 4; Length 36618;	Query Match 25.0%; Score 15; DB 4; Length 36618;
Best Local Similarity 100.0%; Pred. No. 37;	Best Local Similarity 100.0%; Pred. No. 42;	Best Local Similarity 100.0%; Pred. No. 39;	Best Local Similarity 100.0%; Pred. No. 39;
Mismatches 0; Conservative 0; Gaps 0;	Mismatches 0; Conservative 0; Gaps 0;	Mismatches 0; Conservative 0; Gaps 0;	Mismatches 0; Conservative 0; Gaps 0;
QY 22 CACGGTGTACATCC 36	QY 12 CCCCCCTGCTACGG 26	QY 33 ATCCGCCCGGATAC 47	QY 33 ATCCGCCCGGATAC 47
Db 81974 CACGGTGTACATCC 81960	Db 11709 CCCCCCTGCTACGG 11723	Db 1566 ATCCGCCCGGATAC 1552	Db 1566 ATCCGCCCGGATAC 1552
RESULT 13	RESULT 11	RESULT 12	RESULT 12
US-08-930-274-3	US-09-949-016-16935/c	US-09-949-016-16935	US-09-949-016-16935
Sequence 3, Application US/08930274	Sequence 16935, Application US/09949016	Sequence 15, Application US/09664186	Sequence 32, Application US/09497855A
Patent No. 5932441	Patent No. 6812339	Patent No. 6815537	Patent No. 6605432
GENERAL INFORMATION:	GENERAL INFORMATION:	GENERAL INFORMATION:	GENERAL INFORMATION:
APPLICANT:	APPLICANT:	APPLICANT:	APPLICANT:
APPLICANT:	APPLICANT:	APPLICANT:	APPLICANT:
APPLICANT:	APPLICANT:	APPLICANT:	APPLICANT:
TITLE OF INVENTION: VECTORS FOR DIFFERENTIAL EXPRESSION	TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF	TITLE OF INVENTION: Method For Construction Of Thermus-E. coli Shuttle Vectors And Identification Of Two Thermus Plasmid	TITLE OF INVENTION: Polymorphisms In Known Genes Associated With Human Disease, Methods Of Detection And Uses Thereof
NUMBER OF SEQUENCES: 25	NUMBER OF SEQUENCES: 25	NUMBER OF SEQUENCES: 25	NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:	CORRESPONDENCE ADDRESS:	CORRESPONDENCE ADDRESS:	CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.	ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.	ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.	ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., Suite 800	STREET: 2033 K Street, N.W., Suite 800	STREET: 2033 K Street, N.W., Suite 800	STREET: 2033 K Street, N.W., Suite 800
CITY: Washington	CITY: Washington	CITY: Washington	CITY: Washington
STATE: D.C.	STATE: D.C.	STATE: D.C.	STATE: D.C.
COUNTRY: U.S.A.	COUNTRY: U.S.A.	COUNTRY: U.S.A.	COUNTRY: U.S.A.
ZIP: 20006	ZIP: 20006	ZIP: 20006	ZIP: 20006
COMPUTER READABLE FORM:	COMPUTER READABLE FORM:	COMPUTER READABLE FORM:	COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk	MEDIUM TYPE: Floppy disk	MEDIUM TYPE: Floppy disk	MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible	COMPUTER: IBM PC compatible	COMPUTER: IBM PC compatible	COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS	OPERATING SYSTEM: PC-DOS/MS-DOS	OPERATING SYSTEM: PC-DOS/MS-DOS	OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)	SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)	SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)	SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:	CURRENT APPLICATION DATA:	CURRENT APPLICATION DATA:	CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/930,274	APPLICATION NUMBER: US/09/949,016	APPLICATION NUMBER: US/09/664,186	APPLICATION NUMBER: US/09/949,016
FILING DATE: September 29, 1997	FILING DATE: September 29, 1997	FILING DATE: September 29, 1997	FILING DATE: September 29, 1997
PRIOR APPLICATION DATA:	PRIOR APPLICATION DATA:	PRIOR APPLICATION DATA:	PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95302196.1	APPLICATION NUMBER: EP 95302196.1	APPLICATION NUMBER: EP 95302196.1	APPLICATION NUMBER: EP 95302196.1
FILING DATE: 31-MAR-1995	FILING DATE: 31-MAR-1995	FILING DATE: 31-MAR-1995	FILING DATE: 31-MAR-1995
PRIOR APPLICATION DATA:	PRIOR APPLICATION DATA:	PRIOR APPLICATION DATA:	PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB 96/00765	APPLICATION NUMBER: PCT/GB 96/00765	APPLICATION NUMBER: PCT/GB 96/00765	APPLICATION NUMBER: PCT/GB 96/00765
FILING DATE: 29-MAR-1996	FILING DATE: 29-MAR-1996	FILING DATE: 29-MAR-1996	FILING DATE: 29-MAR-1996
ATTORNEY/AGENT INFORMATION:	ATTORNEY/AGENT INFORMATION:	ATTORNEY/AGENT INFORMATION:	ATTORNEY/AGENT INFORMATION:
NAME: Warren M Cheek, Jr.	NAME: Warren M Cheek, Jr.	NAME: Warren M Cheek, Jr.	NAME: Warren M Cheek, Jr.
REGISTRATION NUMBER: 33,367	REGISTRATION NUMBER: 33,367	REGISTRATION NUMBER: 33,367	REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:	REFERENCE/DOCKET NUMBER:	REFERENCE/DOCKET NUMBER:	REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:	TELECOMMUNICATION INFORMATION:	TELECOMMUNICATION INFORMATION:	TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200	TELEPHONE: 202-721-8200	TELEPHONE: 202-721-8200	TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250	TELEFAX: 202-721-8250	TELEFAX: 202-721-8250	TELEFAX: 202-721-8250
TELEX:	TELEX:	TELEX:	TELEX:
INFORMATION FOR SEQ ID NO: 3:	INFORMATION FOR SEQ ID NO: 3:	INFORMATION FOR SEQ ID NO: 3:	INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:	SEQUENCE CHARACTERISTICS:	SEQUENCE CHARACTERISTICS:	SEQUENCE CHARACTERISTICS:
LENGTH: 34 base pairs	LENGTH		

DESCRIPTION: /desc = "synthetic primer"  
US-08-930-274-3

Query Match 23.3%; Score 14; DB 2; Length 34;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TCGACGGCCCCC 17  
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Db 14 TCGACGGCCCCC 27

## RESULT 14

US-08-894-228-9/c  
; Sequence 9, Application US/08894228  
; Patent No. 5914395  
; GENERAL INFORMATION:  
; APPLICANT: PAULIN, DENISE  
; APPLICANT: LI, ZHEN LIN  
; TITLE OF INVENTION: AMPLIFYING SEQUENCES, VECTORS COMPRISING  
; THESE SEQUENCES AND THEIR USES IN COMPOSITIONS FOR THE  
; TITLE OF INVENTION: EXPRESSION OF NUCLEOTIDE SEQUENCES IN TRANSFECTED CELLS,  
; TITLE OF INVENTION: THERAPEUTIC AND VACCINE APPLICATIONS  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR  
; CITY: ARLINGTON  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22202

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/894,228  
FILING DATE: 12-SEP-1997

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/FR96/00261  
FILING DATE: 16-FEB-1996

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 95 01937  
FILING DATE: 20-FEB-1995

ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F.  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 0660-0123-0X PCT  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220

INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 83 base pairs  
TYPE: nucleic acid

STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-894-228-9

Query Match 23.3%; Score 14; DB 2; Length 83;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 38 CCCCCGATACCAGA 51  
|||||  
Db 39 CCCCCGATACCAGA 26

## RESULT 15

US-09-191-521-9/c  
; Sequence 9, Application US/09191521  
; Patent No. 6201115  
; GENERAL INFORMATION:  
; APPLICANT: PAULIN, DENISE  
; APPLICANT: LI, ZHEN LIN

; TITLE OF INVENTION: AMPLIFYING SEQUENCES, VECTORS COMPRISING  
; THESE SEQUENCES AND THEIR USES IN COMPOSITIONS FOR THE  
; EXPRESSION OF NUCLEOTIDE SEQUENCES IN TRANSFECTED CELLS,  
; THERAPEUTIC AND VACCINE APPLICATIONS  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR  
; CITY: ARLINGTON  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22202

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/191,521  
FILING DATE: 13-NOV-1998

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/894,228  
FILING DATE: 12-SEP-1997  
APPLICATION NUMBER: PCT/FR96/00261  
FILING DATE: 16-FEB-1996

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 95 01937  
FILING DATE: 20-FEB-1995

ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F.  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 0660-0123-0X PCT  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220

INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 83 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 9:  
US-09-191-521-9

Query Match 23.3%; Score 14; DB 3; Length 83;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 38 CCCCCGATACCAGA 51  
|||||  
Db 39 CCCCCGATACCAGA 26

Search completed: June 30, 2005, 04:05:09  
Job time : 98.2 secs

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; Sequence 28639, Application US/10282122A  
; Publication No. US20040029129A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Liangsu  
; APPLICANT: Zamudio, Carlos  
; APPLICANT: Malone, Cheryl  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari  
; APPLICANT: Zyekind, Judith  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John  
; APPLICANT: Carr, Grant  
; APPLICANT: Yamamoto, Robert  
; APPLICANT: Forsyth, R.  
; APPLICANT: Xu, H.

; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

; FILE REFERENCE: ELITRA.034A  
; CURRENT APPLICATION NUMBER: US/10/282,122A  
; CURRENT FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/230,335  
; PRIOR FILING DATE: 2000-09-06  
; PRIOR APPLICATION NUMBER: 60/230,347  
; PRIOR FILING DATE: 2000-09-09  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/267,636  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 78614  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 28639  
; LENGTH: 1857  
; TYPE: DNA  
; ORGANISM: Mycobacterium tuberculosis  
US-10-282-122A-28639

Query Match 31.7%; Score 19; DB 17; Length 1857;  
Best Local Similarity 100.0%; Pred. No. 0.64;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCAGCAGCCGACCGCCG 19  
Db 197 GGCAGCAGCCGACCGCCG 179

RESULT 6

US-10-437-963-41853/c  
; Sequence 41853, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 41853  
; LENGTH: 1605  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_4515C.1  
US-10-437-963-41853

Query Match 30.0%; Score 18; DB 19; Length 1605;  
Best Local Similarity 100.0%; Pred. No. 2.3;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CCGCAGCCGCGCACACG 25  
Db 1241 CCGCAGCCGCGCACACG 1224

RESULT 7

US-10-723-860-7061  
; Sequence 7061, Application US/10723860  
; Publication No. US20040253606A1  
; GENERAL INFORMATION:  
; APPLICANT: Aziz, Nataasha  
; APPLICANT: Ginsburg, Wendy M.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &  
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators  
; FILE REFERENCE: 05882.0193.NFUS01  
; CURRENT APPLICATION NUMBER: US/10/723,860  
; CURRENT FILING DATE: 2003-11-26  
; PRIOR APPLICATION NUMBER: 60/429,739  
; PRIOR FILING DATE: 2002-11-26  
; NUMBER OF SEQ ID NOS: 8393  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 7061  
; LENGTH: 3644  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (23)..(23)  
; OTHER INFORMATION: n is a, c, g, or t  
US-10-723-860-7061

Query Match 30.0%; Score 18; DB 20; Length 3644;  
Best Local Similarity 100.0%; Pred. No. 2;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 CAAGCGCGCCAGCACATC 49  
Db 2577 CAAGCGCGCCAGCACATC 2594

RESULT 8

US-09-758-759-164/c  
; Sequence 164, Application US/09758759  
; Publication No. US20040101832A1  
; GENERAL INFORMATION:  
; APPLICANT: Hosted, Thomas J.  
; APPLICANT: Wang, Tim X.  
; APPLICANT: Horan, Ann C.  
; TITLE OF INVENTION: Everninomicin Biosynthetic Genes  
; FILE REFERENCE: ID0983K US  
; CURRENT APPLICATION NUMBER: US/09/758,759  
; CURRENT FILING DATE: 2001-01-11  
; PRIOR APPLICATION NUMBER: US 60/175,751  
; PRIOR FILING DATE: 2000-01-12  
; NUMBER OF SEQ ID NOS: 204  
; SOFTWARE: PatentIn ver. 2.1  
; SEQ ID NO 164

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; LENGTH: 351
; TYPE: DNA
; ORGANISM: Micromonospora carbonacea
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(351)
; OTHER INFORMATION: evck
US-09-758-759-164

Query Match      28.3%; Score 17; DB 11; Length 351;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 GCAGCAGCGCCGCGCC 18
Db      166 GCAGCAGCGCCGCGCC 150

RESULT 9
US-10-437-963-47467/c
; Sequence 47467, Application US/10437963
; Publication No. US2004012334A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 47467
; LENGTH: 1530
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_50232C.1
US-10-437-963-47467

Query Match      28.3%; Score 17; DB 19; Length 1530;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      10 GCACGCGCGCCGCGCGG 26
Db      1152 GCACGCGCGCCGCGCGG 1136

RESULT 10
US-10-156-761-6358
; Sequence 6358, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
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; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 6358
; LENGTH: 2205
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2205)
US-10-156-761-6358

Query Match      28.3%; Score 17; DB 15; Length 2205;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      8 CCGCAGCGCCGCGCAC 24
Db      6 CCGCAGCGCCGCGCAC 22

RESULT 11
US-09-758-759-1
; Sequence 1, Application US/09758759
; Publication No. US20040101832A1
; GENERAL INFORMATION:
; APPLICANT: Hosted, Thomas J.
; APPLICANT: Wang, Tim X.
; APPLICANT: Horan, Ann C.
; TITLE OF INVENTION: Evernimicin Biosynthetic Genes
; FILE REFERENCE: ID0983K US
; CURRENT APPLICATION NUMBER: US/09/758,759
; CURRENT FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: US 60/175,751
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 109519
; TYPE: DNA
; ORGANISM: Micromonospora carbonacea
US-09-758-759-1

Query Match      28.3%; Score 17; DB 11; Length 109519;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 GCAGCAGCGCAGCGCC 18
Db      101991 GCAGCAGCGCAGCGCC 102007

RESULT 12
US-10-156-761-1/c
; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
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; LENGTH: 9025608  
; TYPE: DNA  
; ORGANISM: Streptomyces avermitilis  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (4187715)  
; OTHER INFORMATION: a, t, c, g, other or unknown  
US-10-156-761-1

Query Match 28.3%; Score 17; DB 15; Length 9025608;  
Best Local Similarity 100.0%; Pred. No. 1.7;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 8 CGCACCGCCCGCACAC 24  
|||||  
Db 7654924 CGCACCGCCCGCACAC 7654908

RESULT 13  
US-10-425-115-24623/c  
; Sequence 24623, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 24623  
; LENGTH: 889  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_122463C.1  
US-10-425-115-24623

Query Match 26.7%; Score 16; DB 20; Length 889;  
Best Local Similarity 100.0%; Pred. No. 33;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 5 GCACCGCACCGCCGC 20  
|||||  
Db 358 GCACCGCACCGCCGC 343

RESULT 14  
US-10-437-963-18424/c  
; Sequence 18424, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 18424  
; LENGTH: 1365  
; TYPE: DNA  
; ORGANISM: Oryza sativa

; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_23984C.1  
US-10-437-963-18424

Query Match 26.7%; Score 16; DB 19; Length 1365;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 9 CGCACCGCCCGCACAC 24  
|||||  
Db 995 CGCACCGCCCGCACAC 980

RESULT 15  
US-10-437-963-45329/c  
; Sequence 45329, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 45329  
; LENGTH: 1643  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_48304C.1  
US-10-437-963-45329

Query Match 26.7%; Score 16; DB 19; Length 1643;  
Best Local Similarity 100.0%; Pred. No. 29;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 9 CGCACCGCCCGCACAC 24  
|||||  
Db 508 CGCACCGCCCGCACAC 493

Search completed: June 30, 2005, 04:46:42  
Job time : 273.7 secs

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Result No.	Score	Query Match	Length	DB	ID	Description
1	19	31.7	4403765	3	US-09-103-840A-2	Sequence 2, Appl
2	19	31.7	4411529	3	US-09-103-840A-1	Sequence 1, Appl
3	16	26.7	1191	4	US-09-489-039A-6256	Sequence 6256, Ap
4	16	26.7	1521	4	US-09-489-039A-5599	Sequence 5599, Ap
5	16	26.7	44377	2	US-08-804-227C-7	Sequence 7, Appl
6	16	26.7	44377	2	US-08-804-198-1	Sequence 1, Appl
C 7	15	25.0	373	4	US-09-270-767-26397	Sequence 26397, A
	15	25.0	750	4	US-09-252-991A-13978	Sequence 13978, A
C 8	15	25.0	867	4	US-09-270-767-10912	Sequence 10912, A
C 9	15	25.0	867	4	US-09-252-991A-14155	Sequence 14155, A
C 10	15	25.0	1038	4	US-09-780-049-17	Sequence 17, Appl
C 11	15	25.0	2181	3	US-09-780-049-17	Sequence 17, Appl
C 12	15	25.0	2182	4	US-09-949-016-5543	Sequence 5543, Ap
C 13	15	25.0	2793	2	US-08-347-563A-1	Sequence 1, Appl
C 14	15	25.0	2793	3	US-08-485-942A-1	Sequence 1, Appl
C 15	15	25.0	2793	3	US-08-488-214A-1	Sequence 1, Appl
C 16	15	25.0	2793	3	US-08-488-208A-1	Sequence 1, Appl
C 17	15	25.0	2793	3	US-08-483-211A-1	Sequence 1, Appl
C 18	15	25.0	2793	3	US-08-483-223A-1	Sequence 1, Appl
C 19	15	25.0	2793	3	US-08-438-431A-1	Sequence 1, Appl
C 20	15	25.0	2793	4	US-08-488-225A-1	Sequence 1, Appl
C 21	15	25.0	2793	4	US-09-686-647A-1	Sequence 1, Appl
C 22	15	25.0	2966	3	US-09-780-049-3	Sequence 3, Appl
	15	25.0	3889	2	US-08-648-298-1	Sequence 1, Appl
C 23	15	25.0	3889	2	US-08-648-298-1	Sequence 1, Appl
C 24	15	25.0	5097	4	US-09-902-540-745	Sequence 745, App
C 25	15	25.0	5336	3	US-09-102-528-11	Sequence 11, Appl
C 26	15	25.0	30001	1	US-08-125-468-1	Sequence 1, Appl
C 27	15	25.0	30001	2	US-08-474-933-1	Sequence 1, Appl

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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match      31.7%; Score 19; DB 3; Length 4411529;
Best Local Similarity 100.0%; Pred. No. 0.47;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCAGCAGCCGCGCCGCG 19
    |||||
Db 3362787 GGCAGCAGCCGCGCCGCG 3362805

RESULT 3
US-09-489-039A-6256
; Sequence 6256, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 6256
; LENGTH: 1191
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-6256

Query Match      26.7%; Score 16; DB 4; Length 1191;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 31 ACAAGCGCGCCGACGACA 46
    |||||
Db 1166 ACAAGCGCGCCGACGACA 1181

RESULT 4
US-09-489-039A-5599
; Sequence 5599, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 5599
; LENGTH: 1521
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-5599

Query Match      26.7%; Score 16; DB 4; Length 1521;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 31 ACAAGCGCGCCGACGACA 46
    |||||
Db 1 ACAAGCGCGCCGACGACA 16

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match      31.7%; Score 19; DB 3; Length 4411529;
Best Local Similarity 100.0%; Pred. No. 0.47;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCAGCAGCCGCGCCGCG 19
    |||||
Db 3362787 GGCAGCAGCCGCGCCGCG 3362805

RESULT 5
US-08-804-227C-7
; Sequence 7, Application US/08804227C
; Patent No. 5876991
; GENERAL INFORMATION:
; APPLICANT: DeHoff, Bradley S.
; APPLICANT: Kuhstoss, Stuart A.
; APPLICANT: Rostock, Paul R., Jr.
; APPLICANT: Sutton, Kimberly L.
; TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: THOMAS G. PLANT 1501
; STREET: LILLY CORPORATE CENTER
; CITY: INDIANAPOLIS
; STATE: IN
; COUNTRY: USA
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: ASCII(DOS) Text only
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/804,227C
; FILING DATE: February 21, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Plant, Thomas, G.
; REGISTRATION NUMBER: 35,784
; REFERENCE/DOCKET NUMBER: X-8231
; TELEPHONE: 317-276-2459
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 44377 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 350..14002
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 14046..20036
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 20110..31284
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 31329..36071
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 36155..41830
; US-08-804-227C-7

Query Match      26.7%; Score 16; DB 2; Length 44377;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCAGCAGCCGCGCCGCG 16
    |||||
Db 23338 GGCAGCAGCCGCGCCGCG 23353

RESULT 6
US-08-804-198-1
; Sequence 1, Application US/08804198
; Patent No. 5945320
; GENERAL INFORMATION:
```



APPLICANT: Burgett, Stanley G.  
APPLICANT: Kuhstoss, Stuart A.  
APPLICANT: Rao, Nagaraja R.  
APPLICANT: Richardson, Mark A.  
APPLICANT: Rostock, Paul R., Jr.  
TITLE OF INVENTION: PLATENOLIDE SYNTHASE GENE  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PAUL R. CANTRELL 1138  
STREET: LILLY CORPORATE CENTER  
CITY: INDIANAPOLIS  
STATE: IN  
COUNTRY: USA  
ZIP: 46285  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Macintosh  
OPERATING SYSTEM: Macintosh 7.0  
SOFTWARE: Microsoft Word 5.1  
CURRENT APPLICATION DATA: US/08/804,198  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: CANTRELL, PAUL R.  
REGISTRATION NUMBER: 36,470  
REFERENCE/DOCKET NUMBER: P9113  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 317-276-3885  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 44377 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 350..14002  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 14046..20036  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 20110..31284  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 31329..36071  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 36155..41830  
US-08-804-198-1

Query Match 26.7%; Score 16; DB 2; Length 44377;  
Best Local Similarity 100.0%; Pred. No. 25;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCAGCAGCCGACCGC 16  
Db 23338 GGCAGCAGCCGACCGC 23353

RESULT 7  
US-09-270-767-26397/c  
; Sequence 26397, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517

; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 26397  
; LENGTH: 373  
; TYPE: DNA  
; ORGANISM: *Drosophila melanogaster*  
US-09-270-767-26397

Query Match 25.0%; Score 15; DB 4; Length 373;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 41 CAGACACTCGACCTG 55  
Db 321 CAGACACTCGACCTG 307

RESULT 8  
US-09-252-991A-13978/c  
; Sequence 13978, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 13978  
; LENGTH: 750  
; TYPE: DNA  
; ORGANISM: *Pseudomonas aeruginosa*  
US-09-252-991A-13978

Query Match 25.0%; Score 15; DB 4; Length 750;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GCAGCAGCGCAGCGC 16  
Db 235 GCAGCAGCGCAGCGC 221

RESULT 9  
US-09-270-767-10912/c  
; Sequence 10912, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 10912  
; LENGTH: 867  
; TYPE: DNA  
; ORGANISM: *Drosophila melanogaster*  
US-09-270-767-10912

Query Match 25.0%; Score 15; DB 4; Length 867;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 41 CAGACACTCGACCTG 55  
Db 815 CAGACACTCGACCTG 801

RESULT 10  
US-09-252-991A-14155  
; Sequence 14155, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252.991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 14155  
; LENGTH: 1038  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-14155

Query Match 25.0%; Score 15; DB 4; Length 1038;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GCAGCAGCGCACCGC 16  
Db 882 GCAGCAGCGCACCGC 896  
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RESULT 11  
US-09-780-049-17/c  
; Sequence 17, Application US/09780049  
; Patent No. 6465250  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Jacqueline Wyatt  
; TITLE OF INVENTION: ANTISENSE MODULATION OF PROTEIN PHOSPHATASE 2 CATALYTIC SUBUNIT  
; TITLE OF INVENTION: EXPRESSION  
; FILE REFERENCE: RTS-0134  
; CURRENT APPLICATION NUMBER: US/09/780.049  
; CURRENT FILING DATE: 2001-02-09  
; NUMBER OF SEQ ID NOS: 96  
; SEQ ID NO 17  
; LENGTH: 2181  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (210)...(1139)  
US-09-780-049-17

Query Match 25.0%; Score 15; DB 3; Length 2181;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 CCGCCCGCACACGGG 27  
Db 161 CCGCCCGCACACGGG 147  
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RESULT 12  
US-09-949-016-5543/c  
; Sequence 5543, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949.016

; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5543  
; LENGTH: 2182  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-5543

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Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 CCGCCCGCACACGGG 27  
Db 162 CCGCCCGCACACGGG 148  
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RESULT 13  
US-08-347-563A-1  
; Sequence 1, Application US/08347563A  
; Patent No. 5935810  
; GENERAL INFORMATION:  
; APPLICANT: THE ROCKEFELLER UNIVERSITY  
; TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING NUCLEIC  
; TITLE OF INVENTION: ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Klauber & Jackson  
; STREET: 411 Hackensack Avenue  
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07601

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/347,563A  
; FILING DATE: No. 5935810ember 30, 1994  
; CLASSIFICATION: 514  
; PRIOR APPLICATION NUMBER: 08/292,345  
; FILING DATE: August 17, 1994  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jackson Esq., David A.  
; REGISTRATION NUMBER: 26,742  
; REFERENCE/DOCKET NUMBER: 600-1-087 CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201 487-5800  
; TELEFAX: 201 343-1684  
; TELEX: 133521  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2793 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; DESCRIPTION: Murine ob cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Murine

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; ; FEATURE:
; ; NAME/KEY: CDS
; ; LOCATION: 57..560
US-08-347-563A-1

Query Match      25.0%; Score 15; DB 2; Length 2793;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GCAGCACCGCACC GC 16
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Db       2132 GCAGCACCGCACC GC 2146

RESULT 14
US-08-485-942A-1
; Sequence 1, Application US/08485942A
; Patent No. 6048837
; GENERAL INFORMATION:
; APPLICANT: JEFFREY M. FRIEDMAN, YIYING ZHANG, RICARDO PROENCA,
; APPLICANT: MARGHERITA MAFFEI, JEFFREY HALAAS, KETAN GAJIWALA, AND STEPHEN K. BURLI
; TITLE OF INVENTION: OB POLYPEPTIDE AS MODULATORS OF BODY WEIGHT (AS
; TITLE OF INVENTION: AMENDED)
; NUMBER OF SEQUENCES: 99
; - CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,942A
; FILING DATE: JUNE 7, 1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/438,431
; FILING DATE: May 10, 1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/347,563
; FILING DATE: No. 6048837ember 30, 1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/292,345
; FILING DATE: August 17, 1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-087 CIP 2F
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2793 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; DESCRIPTION: Murine ob cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Murine
; FEATURE:

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; NAME/KEY: CDS
; LOCATION: 57..560
; US-08-485-942A-1

Query Match 25.0%; Score 15; DB 3; Length 2793;
Best Local Similarity 100.0%; Pred.No.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCAGCACCGCACCGC 16
Db 2132 GCAGCACCGCACCGC 2146
|||||
|||||

RESULT 15
US-08-488-214A-1
; Sequence 1, Application US/08488214A
; Patent No. 6124439
; GENERAL INFORMATION:
; APPLICANT: JEFFREY M. FRIEDMAN, YIYING ZHANG, RICARDO PROENCA, AND STEPHEN
; APPLICANT: MARGHERITA MAFFEI, JEFFREY HALAAS, KETAN GAJIWALA, AND STEPHEN
; TITLE OF INVENTION: OB POLYPEPTIDE ANTIBODIES AND METHOD OF MAKING
; TITLE OF INVENTION: (AS AMENDED)
; NUMBER OF SEQUENCES: 99
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,214A
; FILING DATE: JUNE 7, 1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/438,431
; FILING DATE: May 10, 1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/347,563
; FILING DATE: No. 6124439ember 30, 1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/292,345
; FILING DATE: August 17, 1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-087 CIP 2D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2793 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; DESCRIPTION: Murine ob cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Murine
; FEATURE:
; NAME/KEY: CDS

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; LOCATION: 57..560
US-08-488-214A-1
Query Match      25.0%; Score 15; DB 3; Length 2793;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      2 GCAGCACCACCGC 16
        |||||
Db      2132 GCAGCACCACCGC 2146

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Job time : 122.2 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 29, 2005, 19:26:35 ; Search time 51.2 Seconds  
(without alignments)  
1917.512 Million cell updates/sec

Title: US-10-057-136-9  
Perfect score: 60  
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Searched: 1202784 seqs, 818138359 residues

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Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

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  - 3: /cgm2\_6/ptodata/1/ina/6A\_COMB.seq.\*
  - 4: /cgm2\_6/ptodata/1/ina/6B\_COMB.seq.\*
  - 5: /cgm2\_6/ptodata/1/ina/PCTUS\_COMB.seq.\*
  - 6: /cgm2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C 2	16	26.7	1191	US-09-489-039A-6256	Sequence 6256, Ap
C 3	16	26.7	1521	US-09-489-039A-5599	Sequence 5599, Ap
C 4	16	26.7	5262	US-09-902-540-766	Sequence 766, App
C 5	15	25.0	144	US-09-270-767-28122	Sequence 28122, A
C 6	15	25.0	373	US-09-270-767-26397	Sequence 26397, A
C 7	15	25.0	428	US-09-270-767-4535	Sequence 4535, Ap
C 8	15	25.0	428	US-09-270-767-19817	Sequence 19817, A
C 9	15	25.0	601	US-09-949-016-140342	Sequence 140342, A
C 10	15	25.0	770	US-09-270-767-12366	Sequence 12366, A
C 11	15	25.0	867	US-09-270-767-10912	Sequence 10912, A
C 12	15	25.0	1011	US-09-902-540-4174	Sequence 4174, Ap
C 13	15	25.0	1114	US-09-902-540-5466	Sequence 5466, Ap
C 14	15	25.0	2843	US-09-902-540-5195	Sequence 5195, Ap
C 15	15	25.0	3540	US-09-489-039A-6639	Sequence 6639, Ap
C 16	15	25.0	3889	US-08-648-298-1	Sequence 1, Appl
C 17	15	25.0	5336	US-09-102-528-11	Sequence 11, Appl
C 18	15	25.0	13214	US-09-949-016-14015	Sequence 14015, A
C 19	15	25.0	22301	US-09-902-540-1208	Sequence 1208, Ap
C 20	15	25.0	26492	US-09-902-540-1234	Sequence 1234, Ap
C 21	15	25.0	29899	US-09-902-540-1265	Sequence 1265, Ap
C 22	15	25.0	34199	US-09-902-540-1255	Sequence 1255, Ap
C 23	15	25.0	80858	US-09-949-016-12659	Sequence 12659, A
C 24	15	25.0	80859	US-09-949-016-15715	Sequence 15715, A
C 25	15	25.0	536165	US-09-214-808-1	Sequence 1, Appl
C 26	14	23.3	263	US-09-902-540-5928	Sequence 5928, Ap
C 27	14	23.3	285	US-09-513-999C-9020	Sequence 9020, Ap

ALIGNMENTS

RESULT 1

US-09-902-540-7732/C  
; Sequence 7732, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; CURRENT FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; PRIOR FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 7732  
; LENGTH: 756  
; TYPE: DNA  
; ORGANISM: Myxococcus xanthus  
US-09-902-540-7732

Query Match 26.7%; Score 16; DB 4; Length 756;  
Best Local Similarity 100.0%; Pred. No. 25;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 AGTACCGCTCCACCTG 19  
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Db 718 AGTACCGCTCCACCTG 703

RESULT 2

US-09-489-039A-6256  
; Sequence 6256, Application US/09489039A  
; Patent No. 6610836  
; GENERAL INFORMATION:  
; APPLICANT: Gary Breton et. al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
; FILE REFERENCE: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 2709.2004001  
; CURRENT APPLICATION NUMBER: US/09/489,039A  
; CURRENT FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: US 60/117,747  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 14342  
; SEQ ID NO 6256  
; LENGTH: 1191  
; TYPE: DNA  
; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-6256

Sequence 749, Appl  
Sequence 5, Appl  
Sequence 5, Appl  
Sequence 468, Appl  
Sequence 2317, Ap  
Sequence 5362, Ap  
Sequence 3, Appl  
Sequence 2597, Ap  
Sequence 469, App  
Sequence 78057, A  
Sequence 127493,  
Sequence 127494,  
Sequence 152709,  
Sequence 5943, Ap  
Sequence 30, Appl  
Sequence 31, Appl  
Sequence 32, Appl  
Sequence 33, Appl

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Query Match      26.7%; Score 16; DB 4; Length 1191;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 31 ACAAGCGCGCCAGACA 46
Db 1166 ACAAGCGCGCCAGACA 1181

RESULT 3
US-09-489-039A-5599
; Sequence 5599, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 5599
; LENGTH: 1521
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-5599

Query Match      26.7%; Score 16; DB 4; Length 1521;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 31 ACAAGCGCGCCAGACA 46
Db 1 ACAAGCGCGCCAGACA 16

RESULT 4
US-09-902-540-766/c
; Sequence 766, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: MYXOCOCCUS XANTHUS Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 766
; LENGTH: 5262
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-766

Query Match      26.7%; Score 16; DB 4; Length 5262;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AGTACCGCTCCACCTG 19
Db 2441 AGTACCGCTCCACCTG 2426

RESULT 5
US-09-270-767-28122
; Sequence 28122, Application US/09270767
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; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28122
; LENGTH: 144
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-28122

Query Match      25.0%; Score 15; DB 4; Length 144;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CCGCTCCACCTGCAC 22
Db 7 CCGCTCCACCTGCAC 21

RESULT 6
US-09-270-767-26397/c
; Sequence 26397, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26397
; LENGTH: 373
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-26397

Query Match      25.0%; Score 15; DB 4; Length 373;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 41 CAGACACTCGACCTG 55
Db 321 CAGACACTCGACCTG 307

RESULT 7
US-09-270-767-4535
; Sequence 4535, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4535
; LENGTH: 428
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-4535

Query Match      25.0%; Score 15; DB 4; Length 428;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 10 GCTCCACCTGCACAC 24
Db 92 GCTCCACCTGCACAC 106

RESULT 8
US-09-270-767-19817
; Sequence 19817, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19817
; LENGTH: 428
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-19817

Query Match 25.0%; Score 15; DB 4; Length 428;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GCTCCACCTGCACAC 24
Db 92 GCTCCACCTGCACAC 106

RESULT 9
US-09-949-016-140342
; Sequence 140342, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 140342
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-140342

Query Match 25.0%; Score 15; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 TGCACACGGGTGCAC 32
Db 28 TGCACACGGGTGCAC 42

RESULT 10
US-09-270-767-12366
; Sequence 12366, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
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; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12366
; LENGTH: 770
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-12366

Query Match 25.0%; Score 15; DB 4; Length 770;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CCGCTCCACCTGCAC 22
Db 7 CCGCTCCACCTGCAC 21

RESULT 11
US-09-270-767-10912/c
; Sequence 10912, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10912
; LENGTH: 867
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-10912

Query Match 25.0%; Score 15; DB 4; Length 867;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 41 CAGACACTCGACCTG 55
Db 815 CAGACACTCGACCTG 801

RESULT 12
US-09-902-540-4174/c
; Sequence 4174, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 4174
; LENGTH: 1011
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-4174

Query Match 25.0%; Score 15; DB 4; Length 1011;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 8 CCGCTCCACCTGCAC 22  
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Db 60 CCGCTCCACCTGCAC 46

RESULT 13  
US-09-902-540-5466/c  
; Sequence 5466, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; CURRENT FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; PRIOR FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 5466  
; LENGTH: 1114  
; TYPE: DNA  
; ORGANISM: Myxococcus xanthus  
US-09-902-540-5466

Query Match 25.0%; Score 15; DB 4; Length 1114;  
Best Local Similarity 100.0%; Pred. No. 84;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AGTACCGCTCCACCT 18  
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Db 878 AGTACCGCTCCACCT 864

RESULT 14  
US-09-902-540-5195/c  
; Sequence 5195, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; CURRENT FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; PRIOR FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 5195  
; LENGTH: 2843  
; TYPE: DNA  
; ORGANISM: Myxococcus xanthus  
US-09-902-540-5195

Query Match 25.0%; Score 15; DB 4; Length 2843;  
Best Local Similarity 100.0%; Pred. No. 82;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GTACCGCTCCACCTG 19  
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Db 2078 GTACCGCTCCACCTG 2064

RESULT 15  
US-09-489-039A-6639  
; Sequence 6639, Application US/09489039A  
; Patent No. 6610836  
; GENERAL INFORMATION:  
; APPLICANT: Gary Breton et. al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 2709.2004001  
; CURRENT APPLICATION NUMBER: US/09/489,039A  
; CURRENT FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: US 60/117,747  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 14342  
; SEQ ID NO 6639  
; LENGTH: 3540  
; TYPE: DNA  
; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-6639

Query Match 25.0%; Score 15; DB 4; Length 3540;  
Best Local Similarity 100.0%; Pred. No. 82;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAAGTACCGCTCCA 15  
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Db 1851 GGAAGTACCGCTCCA 1865

Search completed: June 30, 2005, 04:06:54  
Job time : 85.2 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 29, 2005, 23:23:45 ; Search time 230.7 Seconds  
(without alignments)  
1625.622 Million cell updates/sec

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Perfect score: 60  
Sequence: 1 ggaagaccctccactgc.....cagacactgactgcgcca 60

Scoring table: ~~OMFGONUC~~  
Gapop 60.0, Gapext 60.0

Searched: 6067389 seqs, 3125258755 residues

Word size : 0

Total number of hits satisfying chosen parameters: 12134778

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq.\*
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- 6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq.\*
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- 8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq.\*
- 9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq.\*
- 10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq.\*
- 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq.\*
- 12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq.\*
- 13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq.\*
- 14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq.\*
- 15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq.\*
- 16: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq.\*
- 17: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq.\*
- 18: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq.\*
- 19: /cgn2\_6/ptodata/1/pubpna/US10G\_PUBCOMB.seq.\*
- 20: /cgn2\_6/ptodata/1/pubpna/US10H\_PUBCOMB.seq.\*
- 21: /cgn2\_6/ptodata/1/pubpna/US10I\_PUBCOMB.seq.\*
- 22: /cgn2\_6/ptodata/1/pubpna/US10J\_PUBCOMB.seq.\*
- 23: /cgn2\_6/ptodata/1/pubpna/US11A\_PUBCOMB.seq.\*
- 24: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq.\*
- 25: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*
- 26: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	60	100.0	60	14	US-10-057-136-9 Sequence 9, Appli
2	60	100.0	2297	17	US-10-406-317-41 Sequence 41, Appl
3	42	70.0	60	14	US-10-057-136-8 Sequence 8, Appli
4	18	30.0	3423	17	US-10-282-122A-40295 Sequence 40295, A
5	18	30.0	3644	20	US-10-723-860-7061 Sequence 7061, Ap
6	17	28.3	903	16	US-10-102-239-2 Sequence 2, Appli
7	17	28.3	1056	16	US-10-102-239-3 Sequence 3, Appli

Query Match 100.0%; Score 60; DB 14; Length 60;

8	17	28.3	4451	16	US-10-102-239-1	Sequence 1, Appli
c 9	17	28.3	2256646	19	US-10-470-565-1	Sequence 1, Appli
c 10	16	26.7	1676	18	US-10-425-114-13259	Sequence 13259, A
c 11	16	26.7	2781	18	US-10-424-599-106970	Sequence 106970, A
c 12	16	26.7	2731748	19	US-10-297-465A-1	Sequence 1, Appli
c 13	16	26.7	2731748	19	US-10-297-465A-1	Sequence 1, Appli
c 14	15	25.0	277	20	US-10-357-930-7109	Sequence 7109, Ap
c 15	15	25.0	297	19	US-10-437-963-94547	Sequence 94547, A
c 16	15	25.0	313	10	US-09-803-719-1076	Sequence 1076, Ap
c 17	15	25.0	336	17	US-10-242-535A-57308	Sequence 57308, A
c 18	15	25.0	336	18	US-10-085-783A-57308	Sequence 57308, A
c 19	15	25.0	396	9	US-09-983-965-4510	Sequence 4510, Ap
c 20	15	25.0	399	9	US-09-983-965-5245	Sequence 5245, Ap
c 21	15	25.0	410	9	US-09-983-965-4484	Sequence 4484, Ap
c 22	15	25.0	428	9	US-09-983-965-5222	Sequence 5222, Ap
c 23	15	25.0	432	20	US-10-357-930-37078	Sequence 37078, A
c 24	15	25.0	438	20	US-10-425-115-118012	Sequence 118012, A
c 25	15	25.0	441	17	US-10-369-493-37815	Sequence 37815, A
c 26	15	25.0	455	13	US-10-027-632-46136	Sequence 46136, A
c 27	15	25.0	455	17	US-10-027-632-46136	Sequence 46136, A
c 28	15	25.0	508	16	US-10-029-386-6481	Sequence 6481, Ap
c 29	15	25.0	508	16	US-10-029-386-11465	Sequence 11465, A
c 30	15	25.0	540	17	US-10-369-493-38565	Sequence 38565, A
c 31	15	25.0	552	17	US-10-369-493-38134	Sequence 38134, A
c 32	15	25.0	620	21	US-10-643-775-638	Sequence 638, App
c 33	15	25.0	622	9	US-09-764-877-1022	Sequence 1022, Ap
c 34	15	25.0	622	17	US-10-242-515-1022	Sequence 1022, Ap
c 35	15	25.0	637	19	US-10-767-701-26630	Sequence 26630, A
c 36	15	25.0	825	20	US-10-425-115-21864	Sequence 21864, A
c 37	15	25.0	975	19	US-10-437-963-90300	Sequence 90300, A
c 38	15	25.0	1040	18	US-10-424-599-106969	Sequence 106969, A
c 39	15	25.0	1066	19	US-10-437-963-75417	Sequence 75417, A
c 40	15	25.0	1093	17	US-10-369-493-43317	Sequence 43217, A
c 41	15	25.0	1182	18	US-10-424-599-49049	Sequence 49049, A
c 42	15	25.0	1186	17	US-10-398-221-1748	Sequence 1748, Ap
c 43	15	25.0	1188	17	US-10-282-122A-12241	Sequence 12241, A
c 44	15	25.0	1262	18	US-10-425-114-34238	Sequence 34238, A
c 45	15	25.0	1304	20	US-10-739-930-3223	Sequence 3223, Ap

## ALIGNMENTS

RESULT 1  
US-10-057-136-9  
; Sequence 9, Application US/10057136  
; Publication No. US20030021770A1  
; GENERAL INFORMATION:  
; APPLICANT: SCHLOM, JEFFREY  
; APPLICANT: KANTOR, JUDITH  
; APPLICANT: KUFE, DONALD  
; APPLICANT: PANICALI, DENNIS  
; APPLICANT: GRITZ, LINDA  
; TITLE OF INVENTION: RECOMBINANT POX VIRUS FOR IMMUNIZATION AGAINST MUC1  
; TITLE OF INVENTION: TUMOR-ASSOCIATED ANTIGEN  
; FILE REFERENCE: 700953/47113C  
; CURRENT APPLICATION NUMBER: US/10/057,136  
; CURRENT FILING DATE: 2002-01-25  
; PRIOR APPLICATION NUMBER: 09/366,670  
; PRIOR FILING DATE: 1999-08-03  
; PRIOR APPLICATION NUMBER: PCT/US98/03693  
; PRIOR FILING DATE: 1998-02-24  
; PRIOR APPLICATION NUMBER: 60/038,253  
; PRIOR FILING DATE: 1997-02-24  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 9  
; LENGTH: 60  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-057-136-9

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; ORGANISM: Homo sapiens
US-10-057-136-8

Query Match      70.0%; Score 42; DB 14; Length 60;
Best Local Similarity 100.0%; Pred. No. 1.7e-13;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 GCACGCGGGTCAACAGCGCGCCAGACACTCGACCTGCGCCA 60
Db 19 GCACGCGGGTCAACAGCGCGCCAGACACTCGACCTGCGCCA 60

RESULT 4
US-10-282-122A-40295
; Sequence 40295, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40295
; LENGTH: 3423
; TYPE: DNA
; ORGANISM: Treponema pallidum
US-10-282-122A-40295

Query Match      30.0%; Score 18; DB 17; Length 3423;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CGCTCCACCTGACACGG 26
Db 1052 CGCTCCACCTGACACGG 1069

RESULT 5
US-10-723-860-7061
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; ORGANISM: Homo sapiens
US-10-057-136-8

Query Match      70.0%; Score 42; DB 14; Length 60;
Best Local Similarity 100.0%; Pred. No. 1.7e-13;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 GCACGCGGGTCAACAGCGCGCCAGACACTCGACCTGCGCCA 60
Db 19 GCACGCGGGTCAACAGCGCGCCAGACACTCGACCTGCGCCA 60

RESULT 4
US-10-282-122A-40295
; Sequence 40295, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40295
; LENGTH: 3423
; TYPE: DNA
; ORGANISM: Treponema pallidum
US-10-282-122A-40295

Query Match      30.0%; Score 18; DB 17; Length 3423;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CGCTCCACCTGACACGG 26
Db 1052 CGCTCCACCTGACACGG 1069

RESULT 5
US-10-723-860-7061
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; Sequence 7061, Application US/10723860  
; Publication No. US20040253606A1  
; GENERAL INFORMATION:  
; APPLICANT: Aziz, Natasha  
; APPLICANT: Ginsburg, Wendy M.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &  
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators  
; FILE REFERENCE: 05882-0193.NFUS01  
; CURRENT APPLICATION NUMBER: US/10/723,860  
; PRIOR FILING DATE: 2003-11-26  
; PRIOR APPLICATION NUMBER: 60/429,739  
; PRIOR FILING DATE: 2002-11-26  
; NUMBER OF SEQ ID NOS: 8393  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 7061  
; LENGTH: 3644  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (23)..(23)  
; OTHER INFORMATION: n is a, c, g, or t  
US-10-723-860-7061

Query Match 30.0%; Score 18; DB 20; Length 3644;  
Best Local Similarity 100.0%; Pred. No. 2.2;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 CAAGCGCGCCAGACACTC 49  
DB 2577 CAAGCGCGCCAGACACTC 2594  
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## RESULT 6

US-10-102-239-2  
; Sequence 2, Application US/10102239  
; Publication No. US20030194790A1  
; GENERAL INFORMATION:  
; APPLICANT: Gesellschaft fuer Biotechnologische Forschung  
; APPLICANT: Deckwer, Wolf-Dieter  
; APPLICANT: Mueller, Rolf-Joachim  
; APPLICANT: van den Heuvel, Joop  
; APPLICANT: Kleeberg, Ilona  
; APPLICANT: Widow, Ute  
; TITLE OF INVENTION: DNA-Sequences coding for ester group cleaving enzymes  
; FILE REFERENCE: 930008-2068  
; CURRENT APPLICATION NUMBER: US/10/102,239  
; CURRENT FILING DATE: 2002-12-30  
; PRIOR APPLICATION NUMBER: DE 10030529  
; PRIOR FILING DATE: 2000-06-28  
; PRIOR FILING DATE: 2000-06-28  
; PRIOR FILING DATE: 2000-06-28  
; PRIOR APPLICATION NUMBER: DE 19947286  
; PRIOR FILING DATE: 1999-09-30  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 903  
; TYPE: DNA  
; ORGANISM: Thermomonospora fusca  
US-10-102-239-2

Query Match 28.3%; Score 17; DB 16; Length 903;  
Best Local Similarity 100.0%; Pred. No. 9.8;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AGTACCGCTCCACCTGC 20  
DB 881 AGTACCGCTCCACCTGC 897  
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## RESULT 7

US-10-102-239-2

US-10-102-239-3  
; Sequence 3, Application US/10102239  
; Publication No. US20030194790A1  
; GENERAL INFORMATION:  
; APPLICANT: Gesellschaft fuer Biotechnologische Forschung  
; APPLICANT: Deckwer, Wolf-Dieter  
; APPLICANT: Mueller, Rolf-Joachim  
; APPLICANT: van den Heuvel, Joop  
; APPLICANT: Kleeberg, Ilona  
; APPLICANT: Widow, Ute  
; TITLE OF INVENTION: DNA-Sequences coding for ester group cleaving enzymes  
; FILE REFERENCE: 930008-2068  
; CURRENT APPLICATION NUMBER: US/10/102,239  
; CURRENT FILING DATE: 2002-12-30  
; PRIOR APPLICATION NUMBER: DE 10030529  
; PRIOR FILING DATE: 2000-06-28  
; PRIOR APPLICATION NUMBER: DE 10030529  
; PRIOR FILING DATE: 2000-06-28  
; PRIOR APPLICATION NUMBER: DE 19947286  
; PRIOR FILING DATE: 1999-09-30  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 1056  
; TYPE: DNA  
; ORGANISM: Thermomonospora fusca  
US-10-102-239-3

Query Match 28.3%; Score 17; DB 16; Length 1056;  
Best Local Similarity 100.0%; Pred. No. 9.6;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AGTACCGCTCCACCTGC 20  
DB 1034 AGTACCGCTCCACCTGC 1050  
|||||

## RESULT 8

US-10-102-239-1  
; Sequence 1, Application US/10102239  
; Publication No. US20030194790A1  
; GENERAL INFORMATION:  
; APPLICANT: Gesellschaft fuer Biotechnologische Forschung  
; APPLICANT: Deckwer, Wolf-Dieter  
; APPLICANT: Mueller, Rolf-Joachim  
; APPLICANT: van den Heuvel, Joop  
; APPLICANT: Kleeberg, Ilona  
; APPLICANT: Widow, Ute  
; TITLE OF INVENTION: DNA-Sequences coding for ester group cleaving enzymes  
; FILE REFERENCE: 930008-2068  
; CURRENT APPLICATION NUMBER: US/10/102,239  
; CURRENT FILING DATE: 2002-12-30  
; PRIOR APPLICATION NUMBER: DE 10030529  
; PRIOR FILING DATE: 2000-06-28  
; PRIOR APPLICATION NUMBER: DE 10030529  
; PRIOR FILING DATE: 2000-06-28  
; PRIOR APPLICATION NUMBER: DE 19947286  
; PRIOR FILING DATE: 1999-09-30  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 4451  
; TYPE: DNA  
; ORGANISM: Thermomonospora fusca  
US-10-102-239-1

Query Match 28.3%; Score 17; DB 16; Length 4451;  
Best Local Similarity 100.0%; Pred. No. 7.7;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AGTACCGCTCCACCTGC 20  
DB 2907 AGTACCGCTCCACCTGC 2923  
|||||

```

; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 106970
; LENGTH: 2781
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(2781)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_67609C.1
US-10-424-599-106970

Query Match      26.7%; Score 16; DB 18; Length 2781;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      32 CAAGCGCGCCAGACAC 47
Db      1838 CAAGCGCGCCAGACAC 1823

RESULT 12
US-10-297-465A-1
; Sequence 1, Application US/10297465A
; Publication No. US20040142413A1
; GENERAL INFORMATION:
; APPLICANT: Simpson, Andrew
; APPLICANT: Reinach, Fernando
; APPLICANT: Setubal, Joao
; APPLICANT: Medanis, Joao
; APPLICANT: Arruda, Paulo
; TITLE OF INVENTION: Isolated Genome of Xylella fastidiosa and Uses Thereof
; FILE REFERENCE: PAFESP 202 US (10213376)
; CURRENT APPLICATION NUMBER: US/10/297,465A
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: PCT/IB01/01618
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,906
; PRIOR FILING DATE: 2001-06-17
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 2731748
; TYPE: DNA
; ORGANISM: Xylella fastidiosa
US-10-297-465A-1

Query Match      26.7%; Score 16; DB 19; Length 2731748;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      41 CAGACACTCGACCTGC 56
Db      1834644 CAGACACTCGACCTGC 1834659

RESULT 13
US-10-297-465A-1/c
; Sequence 1, Application US/10297465A
; Publication No. US20040142413A1
; GENERAL INFORMATION:
; APPLICANT: Simpson, Andrew
; APPLICANT: Reinach, Fernando
; APPLICANT: Setubal, Joao
; APPLICANT: Medanis, Joao
; APPLICANT: Arruda, Paulo
US-10-425-114-13259/c
; Sequence 13259, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 13259
; LENGTH: 1676
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: jC-gmle01810054b09_FLI
US-10-425-114-13259

Query Match      26.7%; Score 16; DB 18; Length 1676;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      32 CAAGCGCGCCAGACAC 47
Db      1319 CAAGCGCGCCAGACAC 1304

RESULT 11
US-10-424-599-106970/c
; Sequence 106970, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
US-10-470-565-1/c
; Sequence 1, Application US/10470565
; Publication No. US20040126870A1
; GENERAL INFORMATION:
; APPLICANT: Societe des Produits Nestle S.A.
; TITLE OF INVENTION: NCC2705 - the genome of a Bifidobacterium
; FILE REFERENCE: 80290/WO
; CURRENT APPLICATION NUMBER: US/10/470,565
; CURRENT FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: EP 01102050.0
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2256646
; TYPE: DNA
; ORGANISM: Bifidobacterium longum
US-10-470-565-1

Query Match      28.3%; Score 17; DB 19; Length 2256646;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      13 CCACCTGCACACGGGGT 29
Db      811934 CCACCTGCACACGGGGT 811918

RESULT 10
US-10-425-114-13259/c
; Sequence 13259, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 13259
; LENGTH: 1676
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: jC-gmle01810054b09_FLI
US-10-425-114-13259

Query Match      26.7%; Score 16; DB 18; Length 1676;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      32 CAAGCGCGCCAGACAC 47
Db      1319 CAAGCGCGCCAGACAC 1304

RESULT 11
US-10-424-599-106970/c
; Sequence 106970, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
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; TITLE OF INVENTION: Isolated Genome of Xylella Fastidiosa and Uses Thereof
; FILE REFERENCE: PAPESP 202 US (10213376)
; CURRENT APPLICATION NUMBER: US/10/297,465A
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: PCT/IB01/01618
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,906
; PRIOR FILING DATE: 2001-06-17
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 1
; LENGTH: 2731748
; TYPE: DNA
; ORGANISM: Xylella fastidiosa
US-10-297-465A-1

Query Match      26.7%; Score 16; DB 19; Length 2731748;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      10 GCTCCACCTGCACG 25
      |||||
Db      1053172 GCTCCACCTGCACG 1053157

RESULT 14
US-10-357-930-7109/c
; Sequence 7109, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7109
; LENGTH: 277
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 90, 257
; OTHER INFORMATION: n = A,T,C or G
US-10-357-930-7109
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Query Match      25.0%; Score 15; DB 20; Length 277;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      17 CTGCACACGGGGTCA 31
      |||||
Db      188 CTGCACACGGGGTCA 174
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RESULT 15
US-10-437-963-94547/c
; Sequence 94547, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 94547
; LENGTH: 297
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_92827C.1
US-10-437-963-94547

Query Match      25.0%; Score 15; DB 19; Length 297;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      8 CCGCTCCACCTGCAC 22
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Db      119 CCGCTCCACCTGCAC 105

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Job time : 336.7 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 29, 2005, 19:26:35 ; Search time 51.2 Seconds  
(without alignments)  
1917.512 Million cell updates/sec

Title: US-10-057-136-10

Perfect score: 60

Sequence: 1 gggtcgactgcccctccgcg.....ctgacacaaaggccagcccca 60

Scoring table: ~~MSGO~~NUC

Gapop 60.0 , Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents NA.\*

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- 2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq.\*
- 3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq.\*
- 4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq.\*
- 5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq.\*
- 6: /cgn2\_6/ptodata/1/ina/backfiles.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	30.0	77851	4	US-09-949-016-12508
2	18	30.0	77867	4	US-09-949-016-13211
3	18	30.0	77867	4	US-09-949-016-13212
4	18	30.0	77940	4	US-09-949-016-12509
5	18	30.0	107937	4	US-09-949-016-17192
6	17	28.3	131	4	US-09-513-999C-34492
7	17	28.3	601	4	US-09-949-016-45813
8	17	28.3	601	4	US-09-949-016-45814
9	17	28.3	601	4	US-09-949-016-62835
10	17	28.3	601	4	US-09-949-016-62836
11	17	28.3	601	4	US-09-949-016-82326
12	17	28.3	601	4	US-09-949-016-122478
13	17	28.3	601	4	US-09-949-016-122479
14	17	28.3	601	4	US-09-949-016-122594
15	17	28.3	601	4	US-09-949-016-146921
16	17	28.3	601	4	US-09-949-016-146922
17	17	28.3	601	4	US-09-949-016-154399
18	17	28.3	601	4	US-09-949-016-175414
19	17	28.3	601	4	US-09-949-016-187496
20	17	28.3	28555	4	US-09-949-016-13046
21	17	28.3	30002	4	US-09-949-016-15866
22	17	28.3	31390	4	US-09-949-016-15193
23	17	28.3	43755	4	US-09-949-016-15889
24	17	28.3	63804	4	US-09-949-016-15200
25	17	28.3	92505	4	US-09-949-016-14018
26	17	28.3	98962	4	US-09-949-016-14133
27	17	28.3	102884	4	US-09-949-016-17100

#### ALIGNMENTS

##### RESULT 1

US-09-949-016-12508

; Sequence 12508, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: C1001307

; CURRENT APPLICATION NUMBER: US/09/949.016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 12508

; LENGTH: 77851

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-12508

Query Match 30.0%; Score 18; DB 4; Length 77851;

Best Local Similarity 100.0%; Pred. No. 2.9;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 ATGGTGTGACCTCAGCTC 40

Db 66930 ATGGTGTGACCTCAGCTC 66947

##### RESULT 2

US-09-949-016-13211

; Sequence 13211, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: C1001307

; CURRENT APPLICATION NUMBER: US/09/949.016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

Sequence 13553, A  
Sequence 12317, A  
Sequence 14205, A  
Sequence 15238, A  
Sequence 16066, A  
Sequence 16723, A  
Sequence 1, Appli  
Sequence 12111, A  
Sequence 14516, A  
Sequence 14517, A  
Sequence 14518, A  
Sequence 14519, A  
Sequence 17226, A  
Sequence 17227, A  
Sequence 17228, A  
Sequence 17229, A  
Sequence 16491, A  
Sequence 4743, Ap

28 17 28.3 103792 4 US-09-949-016-13553  
29 17 28.3 103993 4 US-09-949-016-12317  
30 17 28.3 103971 4 US-09-949-016-14205  
31 17 28.3 143644 4 US-09-949-016-15238  
32 17 28.3 143644 4 US-09-949-016-16066  
33 17 28.3 157822 4 US-09-949-016-16723  
34 17 28.3 162450 3 US-09-345-882-1  
35 17 28.3 187848 4 US-09-949-016-12111  
36 17 28.3 203475 4 US-09-949-016-14516  
37 17 28.3 203475 4 US-09-949-016-14517  
38 17 28.3 203475 4 US-09-949-016-14518  
39 17 28.3 203475 4 US-09-949-016-14519  
40 17 28.3 203475 4 US-09-949-016-17226  
41 17 28.3 203475 4 US-09-949-016-17227  
42 17 28.3 203475 4 US-09-949-016-17228  
43 17 28.3 203475 4 US-09-949-016-17229  
44 16 26.7 145 4 US-09-513-999C-16491  
45 16 26.7 307 4 US-09-313-294A-4743

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; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13211
; LENGTH: 77867
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13211

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Query Match 30.0%; Score 18; DB 4; Length 77867;  
Best Local Similarity 100.0%; Pred. No. 2.9;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 ATGGTGTGACCTCAGCTC 40  
|||||  
db 66954 ATGGTGTGACCTCAGCTC 66971

```

RESULT 3
US-09-949-016-13212
; Sequence 13212, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13212
; LENGTH: 77867
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13212

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Query Match 30.0%; Score 18; DB 4; Length 77867;  
Best Local Similarity 100.0%; Pred. No. 2.9;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 ATGGTGTGACCTCAGCTC 40  
|||  
p/b 66954 ATGGTGTGACCTCAGCTC 66971

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RESULT 4
US-09-949-016-12509
Sequence 12509, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12509
LENGTH: 77940

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; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12509

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Query Match          30.0%; Score 18; DB 4; Length 77940;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 23 ATGGTGTGACCTCAGCTC 40  
Dbb 67027 ATGGTGTGACCTCAGCTC 67044

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RESULT 5
US-09-949-016-17192/c
; Sequence 17192, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17192
; LENGTH: 107937
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(107937)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17192

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Query Match      30.0%; Score 18; DB 4; Length 107937;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 23 ATGGTGTGACCTCAGCTC 40  
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Db 33446 ATGGTGTGACCTCAGCTC 33429

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RESULT 6
US-09-513-999C-34492
; Sequence 34492, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 34492
; LENGTH: 131
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-34492

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Query Match 28.3%; Score 17; DB 4; Length 131;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 24 TGGTGTGACCTCAGCTC 40  
Db 40 TGGTGTGACCTCAGCTC 56

RESULT 7  
US-09-949-016-45813/c  
; Sequence 45813, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 45813  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-45813

Query Match 28.3%; Score 17; DB 4; Length 601;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 24 TGGTGTGACCTCAGCTC 40  
Db 395 TGGTGTGACCTCAGCTC 379

RESULT 8  
US-09-949-016-45814/c  
; Sequence 45814, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 45814  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-45814

Query Match 28.3%; Score 17; DB 4; Length 601;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 24 TGGTGTGACCTCAGCTC 40  
Db 563 TGGTGTGACCTCAGCTC 547

RESULT 9  
US-09-949-016-62835/c  
; Sequence 62835, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 62835  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-62835

Query Match 28.3%; Score 17; DB 4; Length 601;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 24 TGGTGTGACCTCAGCTC 40  
Db 405 TGGTGTGACCTCAGCTC 389

RESULT 10  
US-09-949-016-62836/c  
; Sequence 62836, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 62836  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-62836

Query Match 28.3%; Score 17; DB 4; Length 601;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 24 TGGTGTGACCTCAGCTC 40  
Db 459 TGGTGTGACCTCAGCTC 443

```
RESULT 11
US-09-949-016-82326
; Sequence 82326 Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 82326
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-82326

Query Match      28.3%; Score 17; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      24 TGGTGTGACCTCAGCTC 40
Db      184 TGGTGTGACCTCAGCTC 200

RESULT 12
US-09-949-016-122478/c
; Sequence 122478 Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 122478
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-122478

Query Match      28.3%; Score 17; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      24 TGGTGTGACCTCAGCTC 40
Db      203 TGGTGTGACCTCAGCTC 187

RESULT 13
US-09-949-016-122479/c
; Sequence 122479 Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 122479
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-122479
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; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 122479
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-122479

Query Match      28.3%; Score 17; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      24 TGGTGTGACCTCAGCTC 40
Db      280 TGGTGTGACCTCAGCTC 264

RESULT 14
US-09-949-016-122594/c
; Sequence 122594 Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 122594
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-122594

Query Match      28.3%; Score 17; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      24 TGGTGTGACCTCAGCTC 40
Db      502 TGGTGTGACCTCAGCTC 486

RESULT 15
US-09-949-016-146921
; Sequence 146921 Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
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; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 146921
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-146921

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Query Match      28.3%; Score 17; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      42 TGACACAGGCCGCCCC 58
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Db      544 TGACACAGGCCGCCCC 560

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 29, 2005, 23:23:45 ; Search time 230.7 Seconds  
(without alignments)  
1625.622 Million cell updates/sec

Title: US-10-057-136-10  
Perfect score: 60  
Sequence: 1 gggctgactgcctccgcg.....ctgacacagggccagcccca 60

Scoring table: OLIGO\_NUC.

Gapop 60.0 , Gapext 60.0

Searched: 6067389 seqs, 3125258755 residues

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- 13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq.\*
- 14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq.\*
- 15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq.\*
- 16: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq.\*
- 17: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq.\*
- 18: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq.\*
- 19: /cgn2\_6/ptodata/1/pubpna/US10G\_PUBCOMB.seq.\*
- 20: /cgn2\_6/ptodata/1/pubpna/US10H\_PUBCOMB.seq.\*
- 21: /cgn2\_6/ptodata/1/pubpna/US10I\_PUBCOMB.seq.\*
- 22: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq.\*
- 23: /cgn2\_6/ptodata/1/pubpna/US11A\_PUBCOMB.seq.\*
- 24: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq.\*
- 25: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*
- 26: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
1	60	100.0	60	14	US-10-057-136-10
2	60	100.0	2297	17	US-10-406-317-41
3	19	31.7	25	21	US-10-719-993-598560
4	18	30.0	66025	21	US-10-719-993-6945
5	18	30.0	66025	21	US-10-741-600-17868
6	18	30.0	94330	13	US-10-087-192-1222
7	18	30.0	101193	19	US-10-322-281-468

Sequence 10, Appl  
Sequence 41, Appl  
Sequence 598560,  
Sequence 6945, Ap  
Sequence 17868, A  
Sequence 1222, Ap  
Sequence 468, App

Query Match

100.0%; Score 60; DB 14; Length 60;

Sequence 6815, Ap  
Sequence 17676, A  
Sequence 177881,  
Sequence 39890, A  
Sequence 39891, A  
Sequence 40454, A  
Sequence 17906, A  
Sequence 33959, A  
Sequence 33959, A  
Sequence 7463, Ap  
Sequence 3993, Ap  
Sequence 5580, Ap  
Sequence 285842,  
Sequence 197210,  
Sequence 197210,  
Sequence 47724, A  
Sequence 191464,  
Sequence 132379,  
Sequence 132379,  
Sequence 3376, Ap  
Sequence 287, App  
Sequence 2253, Ap  
Sequence 7066, Ap  
Sequence 1385, Ap  
Sequence 1385, Ap  
Sequence 964, App  
Sequence 16, Appl  
Sequence 6979, Ap  
Sequence 97, Appl  
Sequence 756, App  
Sequence 86, Appl  
Sequence 3999, Ap  
Sequence 11, Appl  
Sequence 130, App

## ALIGNMENTS

### RESULT 1

US-10-057-136-10  
; Sequence 10, Application US/10057136  
; Publication No. US20030021770A1  
; GENERAL INFORMATION:  
; APPLICANT: SCHLOM, JEFFREY  
; APPLICANT: KANTOR, JUDITH  
; APPLICANT: KUFE, DONALD  
; APPLICANT: PANICALI, DENNIS  
; APPLICANT: GRITZ, LINDA  
; TITLE OF INVENTION: RECOMBINANT POX VIRUS FOR IMMUNIZATION AGAINST MUC1  
; TITLE OF INVENTION: TUMOR-ASSOCIATED ANTIGEN  
; FILE REFERENCE: 700953/47113C  
; CURRENT FILING DATE: 2002-01-25  
; PRIOR FILING DATE: 1999-08-03  
; PRIOR FILING DATE: 1998-02-24  
; PRIOR FILING DATE: 1997-02-24  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 10  
; LENGTH: 60  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-057-136-10

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Best Local Similarity 100.0%; Pred. No. 1.2e-23;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTCGACTGCCCTCCGGCGCATGGTGTGACCTCAGCTCCTGTGACACAAAGGCCAGCCCCA 60
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Db 1 GGGTCGACTGCCCTCCGGCGCATGGTGTGACCTCAGCTCCTGTGACACAAAGGCCAGCCCCA 60

RESULT 2
US-10-406-317-41
; Sequence 41, Application US/10406317
; Publication No. US20040019195A1
; GENERAL INFORMATION:
; APPLICANT: Schlom, Jeffrey;
; APPLICANT: Hodge, James;
; APPLICANT: Panicali, Dennis
; TITLE OF INVENTION: A recombinant vector expressing multiple constimulatory
; TITLE OF INVENTION: molecules and uses thereof
; FILE REFERENCE: 38163-0189
; CURRENT APPLICATION NUMBER: US/10/406,317
; CURRENT FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: US/09/856,988
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: PCT/US99/26866
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/111,582
; PRIOR FILING DATE: 1998-12-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 2297
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: VECTOR
US-10-406-317-41

Query Match 100.0%; Score 60; DB 17; Length 2297;
Best Local Similarity 100.0%; Pred. No. 6.1e-24;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTCGACTGCCCTCCGGCGCATGGTGTGACCTCAGCTCCTGTGACACAAAGGCCAGCCCCA 60
    |||
Db 766 GGGTCGACTGCCCTCCGGCGCATGGTGTGACCTCAGCTCCTGTGACACAAAGGCCAGCCCCA 825

RESULT 3
US-10-719-900-598560/c
; Sequence 598560, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 598560
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-598560

Query Match 31.7%; Score 19; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 ATGGTGTGACCTCAGCTCC 41
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Db 19 ATGGTGTGACCTCAGCTCC 1

RESULT 4
US-10-719-993-6945
; Sequence 6945, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6945
; LENGTH: 66025
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(66025)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-4)
US-10-719-993-6945

Query Match 30.0%; Score 18; DB 20; Length 66025;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 ATGGTGTGACCTCAGCTC 40
    |||
Db 13490 ATGGTGTGACCTCAGCTC 13507

RESULT 5
US-10-741-600-17868
; Sequence 17868, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17868
; LENGTH: 66025
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(66025)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-4)
US-10-741-600-17868

Query Match 30.0%; Score 18; DB 21; Length 66025;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 ATGGTGTGACCTCAGCTC 40
    |||
Db 13490 ATGGTGTGACCTCAGCTC 13507

RESULT 6
US-10-087-192-1222
; Sequence 1222, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
```

APPLICANT: Engelhard, Eric K.  
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR  
FILE REFERENCE: 52945200122  
CURRENT APPLICATION NUMBER: US/10/087,192  
CURRENT FILING DATE: 2002-03-01  
PRIOR APPLICATION NUMBER: US 09/747,377  
PRIOR FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: US 09/798,586  
PRIOR FILING DATE: 2001-03-02  
NUMBER OF SEQ ID NOS: 2059  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1222  
LENGTH: 94330  
TYPE: DNA  
ORGANISM: Homo sapiens  
NAME/KEY: misc feature  
LOCATION: (1)\_(94330)  
OTHER INFORMATION: n = A,T,C or G  
US-10-087-192-1222

Query Match 30.0%; Score 18; DB 13; Length 94330;  
Best Local Similarity 100.0%; Pred. No. 1.1;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 ATGGTGTGACCTCAGCTC 40  
|||||  
Db 75027 ATGGTGTGACCTCAGCTC 75044

RESULT 7  
US-10-322-281-468  
Sequence 468, Application US/10322281  
Publication No. US20040126762A1  
GENERAL INFORMATION:  
APPLICANT: David W. Morris  
APPLICANT: Marc S. Malandro  
TITLE OF INVENTION: Novel Compositions and Methods in Cancer  
FILE REFERENCE: 529452001000  
CURRENT APPLICATION NUMBER: US/10/322,281  
CURRENT FILING DATE: 2002-12-17  
NUMBER OF SEQ ID NOS: 866  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 468  
LENGTH: 101193  
TYPE: DNA  
ORGANISM: Homo sapiens  
NAME/KEY: misc feature  
LOCATION: (1)\_(101193)  
OTHER INFORMATION: n = A,T,C or G  
US-10-322-281-468

Query Match 30.0%; Score 18; DB 19; Length 101193;  
Best Local Similarity 100.0%; Pred. No. 1.1;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 CCTCAGCTCCTGACACAA 49  
|||||  
Db 59706 CCTCAGCTCCTGACACAA 59723

RESULT 8  
US-10-719-993-6815  
Sequence 6815, Application US/10719993  
Publication No. US20040265849A1  
GENERAL INFORMATION:  
APPLICANT: CARGILL, Michele et al.  
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001496  
CURRENT APPLICATION NUMBER: US/10/719,993

CURRENT FILING DATE: 2003-11-24  
NUMBER OF SEQ ID NOS: 55342  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 6815  
LENGTH: 1980090  
TYPE: DNA  
ORGANISM: Homo sapiens  
NAME/KEY: misc feature  
LOCATION: (1)\_(1980090)  
OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-  
US-10-719-993-6815

Query Match 30.0%; Score 18; DB 20; Length 1980090;  
Best Local Similarity 100.0%; Pred. No. 0.65;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 ATGGTGTGACCTCAGCTC 40  
|||||  
Db 47785 ATGGTGTGACCTCAGCTC 47802

RESULT 9  
US-10-741-600-17676  
Sequence 17676, Application US/10741600  
Publication No. US20050026169A1  
GENERAL INFORMATION:  
APPLICANT: CARGILL, Michele et al.  
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001499  
CURRENT APPLICATION NUMBER: US/10/741,600  
CURRENT FILING DATE: 2003-12-22  
NUMBER OF SEQ ID NOS: 73997  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 17676  
LENGTH: 1980090  
TYPE: DNA  
ORGANISM: Homo sapiens  
NAME/KEY: misc feature  
LOCATION: (1)\_(1980090)  
OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-  
US-10-741-600-17676

Query Match 30.0%; Score 18; DB 21; Length 1980090;  
Best Local Similarity 100.0%; Pred. No. 0.65;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 ATGGTGTGACCTCAGCTC 40  
|||||  
Db 47785 ATGGTGTGACCTCAGCTC 47802

RESULT 10  
US-10-425-115-177881  
Sequence 177881, Application US/10425115  
Publication No. US20040214272A1  
GENERAL INFORMATION:  
APPLICANT: La Rosa, Thomas J.  
APPLICANT: Kovalic, David K.  
APPLICANT: Zhou, Yihua  
APPLICANT: Cao, Yongwei  
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
FILE REFERENCE: 38-21(53222)B  
CURRENT APPLICATION NUMBER: US/10/425,115  
CURRENT FILING DATE: 2003-04-28  
NUMBER OF SEQ ID NOS: 369326  
SEQ ID NO 177881  
LENGTH: 192  
TYPE: DNA  
ORGANISM: Zea mays

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;
; FEATURE:
; OTHER INFORMATION: Clone ID: M8T4577_93815C.1
US-10-425-115-177881

Query Match      28.3%; Score 17; DB 20; Length 192;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 39 TCCTGACACAGGCCAG 55
Db 107 TCCTGACACAGGCCAG 123

RESULT 11
US-10-719-993-39890
; Sequence 39890, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39890
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-39890

Query Match      28.3%; Score 17; DB 20; Length 201;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 TGGTGTGACCTCAGCTC 40
Db 163 TGGTGTGACCTCAGCTC 179

RESULT 12
US-10-719-993-39891
; Sequence 39891, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39891
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-39891

Query Match      28.3%; Score 17; DB 20; Length 201;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 TGGTGTGACCTCAGCTC 40
Db 163 TGGTGTGACCTCAGCTC 179

RESULT 13
US-10-719-993-40454
; Sequence 40454, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40454
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-40454

Query Match      28.3%; Score 17; DB 20; Length 201;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 TGGTGTGACCTCAGCTC 40
Db 85 TGGTGTGACCTCAGCTC 69

RESULT 14
US-10-357-930-17906/c
; Sequence 17906, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17906
; LENGTH: 314
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-357-930-17906

Query Match      28.3%; Score 17; DB 20; Length 314;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 TGGTGTGACCTCAGCTC 40
Db 85 TGGTGTGACCTCAGCTC 69

RESULT 15
US-10-242-535A-33959/c
; Sequence 33959, Application US/10242535A
; Publication No. US20040013663A1
```



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; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liaw, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US 10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 33959
; LENGTH: 318
; TYPE: DNA
; ORGANISM: Human
US-10-242-535A-33959

Query Match      28.3%; Score 17; DB 17; Length 318;
Best Local Similarity 100.0%; Pred.No. 11;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      24 TGGTGTGACCTCAGCTC 40
        |||||
Db      306 TGGTGTGACCTCAGCTC 290

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Search completed: June 30, 2005, 04:50:56  
Job time : 378.7 secs

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Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	18	30.0	4594	4	US-09-112-580-3	Sequence 3, Appli
2	18	30.0	48471	4	US-09-949-016-16416	Sequence 16416, A
3	16	26.7	492	4	US-09-270-767-2029	Sequence 2029, Ap
4	16	26.7	492	4	US-09-270-767-17311	Sequence 17311, A
5	16	26.7	1473	4	US-09-902-540-5372	Sequence 5372, Ap
6	16	26.7	34662	4	US-09-902-540-1261	Sequence 1261, A
7	15	25.0	68	4	US-09-513-999C-18503	Sequence 18503, A
8	15	25.0	284	4	US-09-513-999C-35189	Sequence 35189, A
9	15	25.0	495	4	US-09-270-767-2040	Sequence 2040, Ap
10	15	25.0	495	4	US-09-270-767-17322	Sequence 17322, A
11	15	25.0	601	4	US-09-949-016-131295	Sequence 131295,
12	15	25.0	601	4	US-09-949-016-131297	Sequence 131297,
13	15	25.0	1327	4	US-09-270-957-9	Sequence 9, Appli
14	15	25.0	1386	4	US-09-489-039A-5005	Sequence 5005, Ap
15	15	25.0	1440	4	US-09-270-767-13289	Sequence 12289, A
16	15	25.0	1614	4	US-09-902-540-8389	Sequence 8389, Ap
17	15	25.0	2190	4	US-09-270-767-12310	Sequence 12310, A
18	15	25.0	2503	4	US-09-602-777A-277	Sequence 277, App
19	15	25.0	7186	4	US-09-902-540-879	Sequence 879, App
20	15	25.0	20063	4	US-09-949-016-14176	Sequence 14176, A
21	15	25.0	20520	4	US-09-949-016-14394	Sequence 14394, A
22	15	25.0	51508	4	US-09-949-016-16681	Sequence 16681, A
23	15	25.0	77536	4	US-09-410-551B-1	Sequence 1, Appli
24	15	25.0	77536	4	US-09-410-551B-1	Sequence 1, Appli
25	15	25.0	77536	4	US-09-940-316B-1	Sequence 1, Appli
26	15	25.0	77536	4	US-09-940-316B-1	Sequence 1, Appli
27	15	25.0	199945	4	US-09-949-016-15436	Sequence 15436, A

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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16416
; LENGTH: 48471
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16416

Query Match      30.0%; Score 18; DB 4; Length 48471;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      32 CGTCTGCACCGCACCC 49
      |||||
DB      31062 CGTCTGCACCGCACCC 31079

RESULT 3
US-09-270-767-2029/c
; Sequence 2029, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2029
; LENGTH: 492
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-2029

Query Match      26.7%; Score 16; DB 4; Length 492;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 AACGGCACCTCCAGCA 21
      |||||
DB      350 AACGGCACCTCCAGCA 335

RESULT 4
US-09-270-767-17311/c
; Sequence 17311, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17311
; LENGTH: 492
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-17311

Query Match      26.7%; Score 16; DB 4; Length 492;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 AACGGCACCTCCAGCA 21
      |||||
DB      350 AACGGCACCTCCAGCA 335

RESULT 5
US-09-902-540-5372/c
; Sequence 5372, Application US/09902540

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; PRIOR FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 36681  
; SOFTWARE: Patent.pm  
; SEQ ID NO 18503  
; LENGTH: 68  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 7  
; OTHER INFORMATION: s=g or c  
US-09-513-999C-18503

Query Match 25.0%; Score 15; DB 4; Length 68;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GCACCTCCAGCACAC 24  
Db 64 GCACCTCCAGCACAC 50

## RESULT 8

US-09-513-999C-35189/c  
; Sequence 35189, Application US/09513999C  
; Patent No. 6783961  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclert, A.  
; APPLICANT: Giordano, J.Y.

; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; Patent No. 6783961  
; FILE REFERENCE: 59.US2.REG  
; CURRENT APPLICATION NUMBER: US/09/513,999C  
; CURRENT FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/122,487  
; PRIOR FILING DATE: 1999-02-26

; NUMBER OF SEQ ID NOS: 36681  
; SOFTWARE: Patent.pm  
; SEQ ID NO 35189  
; LENGTH: 284  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 275  
; OTHER INFORMATION: y=c or t  
US-09-513-999C-35189

Query Match 25.0%; Score 15; DB 4; Length 284;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 CCTCCAGCACACGGA 27  
Db 201 CCTCCAGCACACGGA 187

## RESULT 9

US-09-270-767-2040  
; Sequence 2040, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.

; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2040  
; LENGTH: 495  
; TYPE: DNA

; ORGANISM: Drosophila melanogaster  
US-09-270-767-2040

Query Match 25.0%; Score 15; DB 4; Length 495;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 ACGGCACCTCCAGCA 21  
Db 83 ACGGCACCTCCAGCA 97

## RESULT 10

US-09-270-767-17322  
; Sequence 17322, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.

; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 17322  
; LENGTH: 495  
; TYPE: DNA  
; ORGANISM: Drosophila melanogaster  
US-09-270-767-17322

Query Match 25.0%; Score 15; DB 4; Length 495;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 ACGGCACCTCCAGCA 21  
Db 83 ACGGCACCTCCAGCA 97

## RESULT 11

US-09-949-016-131295  
; Sequence 131295, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE; METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 131295  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-131295

Query Match 25.0%; Score 15; DB 4; Length 601;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 CGTCTGCACCCGACA 46  
Db 228 CGTCTGCACCCGACA 242

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RESULT 12
US-09-949-016-131297
; Sequence 131297, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 131297
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-131297

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; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 5005
; LENGTH: 1386
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-5005

Query Match 25.0%; Score 15; DB 4; Length 1386;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AACGGCACCTCCAGC 20 -
Db 1118 AACGGCACCTCCAGC 1104
|||||
|||||

RESULT 15
US-09-270-767-12289/c
; Sequence 12289, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12289
; LENGTH: 1440
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-12289

```

```

; APPLICANT: Richard A. Jefferson and Jorge E. Mayer
; TITLE OF INVENTION: MICROBIAL -GLUCONIDASE GENES, GENE
; TITLE OF INVENTION: PRODUCTS, AND USES THEREOF
; FILE REFERENCE: 190106.405C1
; CURRENT APPLICATION NUMBER: US/09/270,957
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1327
; TYPE: DNA
; ORGANISM: Enterobacter sp. / Salmonella sp.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(1327)
; OTHER INFORMATION: n = A,T,C or G
US-09-270-957-9

Query Match          25.0%;   Score 15;   DB 4;   Length 1327;
Best Local Similarity 100.0%;   Pred. No. 1.le+02;
Matches 15;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

QY      40  CCGGACACCCGGTCCA 54
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Db      731  CCGGACACCCGGTCCA 745

RESULT 14
US-09-489-039A-5005/C
; Sequence 5005, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

```

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 29, 2005, 23:23:45 ; Search time 230.7 Seconds  
(without alignments)  
1625.622 Million cell updates/sec

Title: US-10-057-136-11  
Perfect score: 60  
Sequence: 1 ggttaacggacacccagc.....ccgacacccgtccagtcctcg 60

Scoring table: OPAGO NUC  
Gapop 60.0 , Gapext 60.0

Searched: 6067389 seqs, 3125258755 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 12134778

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications NA:  
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19: /cgn2\_6/ptodata/1/pubpna/US10G\_PUBCOMB.seq:  
20: /cgn2\_6/ptodata/1/pubpna/US10H\_PUBCOMB.seq:  
21: /cgn2\_6/ptodata/1/pubpna/US10I\_PUBCOMB.seq:  
22: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:  
23: /cgn2\_6/ptodata/1/pubpna/US11A\_PUBCOMB.seq:  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	60	100.0	60	14 US-10-057-136-11	Sequence 11, Appl
2	60	100.0	2297	17 US-10-406-317-41	Sequence 41, Appl
C 3	18	30.0	2589	17 US-10-108-260A-909	Sequence 909, App
C 4	18	30.0	12614	17 US-10-242-355-1086	Sequence 1086, App
5	17	28.3	738	18 US-10-425-114-2162	Sequence 1162, Ap
6	17	28.3	2337	18 US-10-425-114-3365	Sequence 3365, A
7	17	28.3	2420	20 US-10-425-115-133325	Sequence 133325,

8	17	28.3	2442	18	US-10-425-114-32585	Sequence 32585, A
9	17	28.3	2442	20	US-10-425-115-133324	Sequence 133324,
C 10	17	28.3	9521	18	US-10-168-663-18	Sequence 18, Appl
11	17	28.3	9521	18	US-10-168-663-19	Sequence 19, Appl
12	16	26.7	29	16	US-10-060-793-35	Sequence 35, Appl
13	16	26.7	70	21	US-10-911-838-71	Sequence 71, Appl
14	16	26.7	70	21	US-10-911-838-81	Sequence 81, Appl
C 15	16	26.7	406	9	US-09-560-863-437	Sequence 437, App
C 16	16	26.7	426	19	US-10-437-963-57337	Sequence 57337, A
C 17	16	26.7	570	13	US-10-027-632-137411	Sequence 137411,
C 18	16	26.7	570	17	US-10-027-632-137411	Sequence 137411,
C 19	16	26.7	577	13	US-10-027-632-65392	Sequence 65392, A
C 20	16	26.7	577	13	US-10-027-632-67359	Sequence 67359, A
C 21	16	26.7	577	17	US-10-027-632-65392	Sequence 65392, A
C 22	16	26.7	577	17	US-10-027-632-67359	Sequence 67359, A
C 23	16	26.7	587	13	US-10-027-632-49543	Sequence 49543, A
C 24	16	26.7	587	17	US-10-027-632-49543	Sequence 49543, A
C 25	16	26.7	629	13	US-10-027-632-164498	Sequence 164498,
C 26	16	26.7	629	17	US-10-027-632-164498	Sequence 164498,
C 27	16	26.7	639	19	US-10-437-963-38249	Sequence 38249, A
C 28	16	26.7	679	13	US-10-027-632-66763	Sequence 66763, A
C 29	16	26.7	679	17	US-10-027-632-66763	Sequence 66763, A
C 30	16	26.7	861	15	US-10-156-761-2432	Sequence 2432, Ap
C 31	16	26.7	1182	16	US-10-060-793-41	Sequence 41, Appl
C 32	16	26.7	1323	17	US-10-282-122A-31341	Sequence 31341, A
C 33	16	26.7	1671	20	US-10-425-115-172468	Sequence 172468,
C 34	16	26.7	1887	20	US-10-425-115-172461	Sequence 172461,
C 35	16	26.7	2050	20	US-10-425-115-172465	Sequence 172465,
C 36	16	26.7	2062	19	US-10-437-963-94245	Sequence 94245, A
C 37	16	26.7	2196	19	US-10-437-963-51097	Sequence 51097, A
C 38	16	26.7	2275	20	US-10-425-115-128087	Sequence 128087, A
C 39	16	26.7	2355	19	US-10-437-963-94248	Sequence 94248, A
C 40	16	26.7	2573	15	US-10-223-085-47	Sequence 47, Appl
C 41	16	26.7	2573	15	US-10-223-084-47	Sequence 47, Appl
C 42	16	26.7	2573	15	US-10-223-088-47	Sequence 47, Appl
C 43	16	26.7	2573	15	US-10-223-090-47	Sequence 47, Appl
C 44	16	26.7	2573	15	US-10-223-087-47	Sequence 47, Appl
C 45	16	26.7	2573	15	US-10-223-083-47	Sequence 47, Appl

ALIGNMENTS

RESULT 1  
US-10-057-136-11  
; Sequence 11, Application US/10057136  
; Publication No. US20030021770A1  
; GENERAL INFORMATION:  
; APPLICANT: SCHLOM, JEFFREY  
; APPLICANT: KANTOR, JUDITH  
; APPLICANT: KUFE, DONALD  
; APPLICANT: PANICALI, DENNIS  
; APPLICANT: GRITZ, LINDA  
; TITLE OF INVENTION: RECOMBINANT POX VIRUS FOR IMMUNIZATION AGAINST MUC1  
; FILE OF INVENTION: TUMOR-ASSOCIATED ANTIGEN  
; FILE REFERENCE: 700953/47113C  
; CURRENT APPLICATION NUMBER: US/10/057,136  
; CURRENT FILING DATE: 2002-01-25  
; PRIOR APPLICATION NUMBER: 09/366,670  
; PRIOR FILING DATE: 1999-08-03  
; PRIOR APPLICATION NUMBER: PCT/US98/03693  
; PRIOR FILING DATE: 1998-02-24  
; PRIOR APPLICATION NUMBER: 60/038,253  
; PRIOR FILING DATE: 1997-02-24  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 11  
; LENGTH: 60  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-057-136-11

Query Match 100.0% Score 60; DB 14; Length 60;

Best Local Similarity 100.0%; Pred. No. 2.8e-24;  
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGTTCACGGCACTCCAGCACACGGAGTCAGTCTGCACACCGACACCCGTCACGCTCCG 60  
Db 1 GGTTCACGGCACTCCAGCACACGGAGTCAGTCTGCACACCGACACCCGTCACGCTCCG 60

RESULT 2  
US-10-406-317-41  
; Sequence 41, Application US/10406317  
; Publication No. US20040019195A1  
; GENERAL INFORMATION:  
; APPLICANT: Schlom, Jeffrey;  
; APPLICANT: Hodge, James;  
; APPLICANT: Panicali, Dennis  
; TITLE OF INVENTION: A recombinant vector expressing multiple constitutulatory  
; TITLE OF INVENTION: molecules and uses thereof  
; FILE REFERENCE: 38163-0189  
; CURRENT APPLICATION NUMBER: US/10/406,317  
; CURRENT FILING DATE: 2003-04-04  
; PRIOR APPLICATION NUMBER: US/09/856,988  
; PRIOR FILING DATE: 2001-05-30  
; PRIOR APPLICATION NUMBER: PCT/US99/26866  
; PRIOR FILING DATE: 1999-11-12  
; PRIOR APPLICATION NUMBER: 60/111,582  
; PRIOR FILING DATE: 1998-12-09  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 41  
; LENGTH: 2297  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: VECTOR  
US-10-406-317-41

Query Match 100.0%; Score 60; DB 17; Length 2297;  
Best Local Similarity 100.0%; Pred. No. 1.7e-24;  
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGTTCACGGCACTCCAGCACACGGAGTCAGTCTGCACACCGACACCCGTCACGCTCCG 60  
Db 826 GGTTCACGGCACTCCAGCACACGGAGTCAGTCTGCACACCGACACCCGTCACGCTCCG 885

RESULT 3  
US-10-108-260A-909/c  
; Sequence 909, Application US/10108260A  
; Publication No. US20040005560A1  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: NO. US20040005560A1e1 full length cDNA  
; FILE REFERENCE: H1-A0106  
; CURRENT APPLICATION NUMBER: US/10/108,260A  
; CURRENT FILING DATE: 2002-03-27  
; NUMBER OF SEQ ID NOS: 5458  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 909  
; LENGTH: 2589  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-108-260A-909

Query Match 30.0%; Score 18; DB 17; Length 2589;  
Best Local Similarity 100.0%; Pred. No. 1.6; Indels 0; Gaps 0;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 6 AACGGCACCTCCAGCACA 23  
Db 1533 AACGGCACCTCCAGCACA 1516

RESULT 4  
US-10-242-355-1086/c  
; Sequence 1086, Application US/10242355  
; Publication No. US20030235831A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PC003C1  
; CURRENT APPLICATION NUMBER: US/10/242,355  
; CURRENT FILING DATE: 2002-09-13  
; PRIOR APPLICATION NUMBER: 09/764,897  
; PRIOR FILING DATE: 2001-01-17  
; PRIOR APPLICATION NUMBER: 60/179,065  
; PRIOR FILING DATE: 2000-01-31  
; PRIOR APPLICATION NUMBER: 60/180,628  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: 60/214,886  
; PRIOR FILING DATE: 2000-06-28  
; PRIOR APPLICATION NUMBER: 60/217,487  
; PRIOR FILING DATE: 2000-07-11  
; PRIOR APPLICATION NUMBER: 60/225,758  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/220,963  
; PRIOR FILING DATE: 2000-07-26  
; PRIOR APPLICATION NUMBER: 60/217,496  
; PRIOR FILING DATE: 2000-07-11  
; PRIOR APPLICATION NUMBER: 60/225,447  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/218,290  
; PRIOR FILING DATE: 2000-07-14  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 1267  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1086  
; LENGTH: 12614  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-242-355-1086

Query Match 30.0%; Score 18; DB 17; Length 12614;  
Best Local Similarity 100.0%; Pred. No. 1.3;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 6 AACGGCACCTCCAGCACA 23  
Db 2885 AACGGCACCTCCAGCACA 2868

RESULT 5  
US-10-425-114-2162  
; Sequence 2162, Application US/10425114  
; Publication No. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E  
; APPLICANT: Tabaska, Jack E  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 2162  
; LENGTH: 738  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 700205315\_FLI  
US-10-425-114-2162



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Query Match      28.3%; Score 17; DB 18; Length 738;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 GTTCAACGGCACCTCCA 18
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Db      58 GTTCAACGGCACCTCCA 74

RESULT 6
US-10-425-114-33665
; Sequence 33665, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 33665
; LENGTH: 2337
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLM017156D10_FLI
US-10-425-114-33665

Query Match      28.3%; Score 17; DB 18; Length 2337;
Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 GTTCAACGGCACCTCCA 18
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Db      1657 GTTCAACGGCACCTCCA 1673

RESULT 7
US-10-425-115-133325
; Sequence 133325, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 133325
; LENGTH: 2420
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_53081C.1
US-10-425-115-133325

Query Match      28.3%; Score 17; DB 20; Length 2420;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 GTTCAACGGCACCTCCA 18
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Db      1657 GTTCAACGGCACCTCCA 1673

RESULT 8
US-10-425-114-32585
; Sequence 32585, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 32585
; LENGTH: 2442
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLM017006E01_FLI
US-10-425-114-32585

Query Match      28.3%; Score 17; DB 18; Length 2442;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 GTTCAACGGCACCTCCA 18
      |||||
Db      1762 GTTCAACGGCACCTCCA 1778

RESULT 9
US-10-425-115-133324
; Sequence 133324, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 133324
; LENGTH: 2442
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_53080C.1
US-10-425-115-133324

Query Match      28.3%; Score 17; DB 20; Length 2442;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 GTTCAACGGCACCTCCA 18
      |||||
Db      1762 GTTCAACGGCACCTCCA 1778

RESULT 10
US-10-168-663-18/c
; Sequence 18, Application US/10168663
; Publication No. US2004008692A1
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; GENERAL INFORMATION:
; APPLICANT: Plant Bioscience Limited
; APPLICANT: Chater, Keith F
; APPLICANT: Bruton, Celia J
; APPLICANT: O'Rourke, Sean J
; APPLICANT: Wietzorrek, Andreas W
; TITLE OF INVENTION: Methods and Materials Relating to Gene Expression
; FILE REFERENCE: 0380-P02909US0
; CURRENT APPLICATION NUMBER: US/10/168,663
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: PCT/GS00/04972
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: GB 9930477.6
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18
; LENGTH: 9521
; TYPE: DNA
; ORGANISM: Streptomyces coelicolor
US-10-168-663-18

Query Match      28.3%; Score 17; DB 18; Length 9521;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 CAACGGCACCTCCAGCA 21
Db      5271 CAACGGCACCTCCAGCA 5255

RESULT 11
US-10-168-663-19
; Sequence 19, Application US/10168663
; Publication No. US20040086962A1
; GENERAL INFORMATION:
; APPLICANT: Plant Bioscience Limited
; APPLICANT: Chater, Keith F
; APPLICANT: Bruton, Celia J
; APPLICANT: O'Rourke, Sean J
; APPLICANT: Wietzorrek, Andreas W
; TITLE OF INVENTION: Methods and Materials Relating to Gene Expression
; FILE REFERENCE: 0380-P02909US0
; CURRENT APPLICATION NUMBER: US/10/168,663
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: PCT/GS00/04972
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: GB 9930477.6
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
; LENGTH: 9521
; TYPE: DNA
; ORGANISM: Streptomyces coelicolor
US-10-168-663-19

Query Match      28.3%; Score 17; DB 18; Length 9521;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 CAACGGCACCTCCAGCA 21
Db      4251 CAACGGCACCTCCAGCA 4267

RESULT 12
US-10-060-793-35
; Sequence 35, Application US/10060793
; Publication No. US20030196217A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
```

```
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: DESATURASE GENES, ENZYMES ENCODED
; TITLE OF INVENTION: THEREBY, AND USES THEREOF
; FILE REFERENCE: 6884.US-01
; CURRENT APPLICATION NUMBER: US/10/060,793
; CURRENT FILING DATE: 2002-06-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Forward Primer RO975
US-10-060-793-35

Query Match      26.7%; Score 16; DB 16; Length 29;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      12 ACCTCCAGCACACGGA 27
Db      6 ACCTCCAGCACACGGA 21

RESULT 13
US-10-911-838-71
; Sequence 71, Application US/10911838
; Publication No. US20050069869A1
; GENERAL INFORMATION:
; APPLICANT: AMBROSINO, Donna
; APPLICANT: HERNANDEZ, Hector
; APPLICANT: GREENOUGH, Thomas
; APPLICANT: LUZURIAGA, Katherine
; APPLICANT: SOMASUNDARAN, Mohan
; APPLICANT: BABCOCK, Gregory J.
; APPLICANT: THOMAS, JR., William D.
; APPLICANT: SULLIVAN, John
; TITLE OF INVENTION: SARS NUCLEIC ACIDS, PROTEINS, ANTIBODIES
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: MJ1-002
; CURRENT APPLICATION NUMBER: US/10/911,838
; CURRENT FILING DATE: 2004-08-04
; PRIOR APPLICATION NUMBER: US 60/565595
; PRIOR FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: US 60/545670
; PRIOR FILING DATE: 2004-02-18
; PRIOR APPLICATION NUMBER: US 60/510251
; PRIOR FILING DATE: 2003-10-09
; PRIOR APPLICATION NUMBER: US 60/492529
; PRIOR FILING DATE: 2003-08-04
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 71
; LENGTH: 70
; TYPE: DNA
; ORGANISM: SARS-Associated Coronavirus
US-10-911-838-71

Query Match      26.7%; Score 16; DB 21; Length 70;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 GTTCACGGCACCTCC 17
Db      1 GTTCACGGCACCTCC 16

RESULT 14
US-10-911-838-81/c
; Sequence 81, Application US/10911838
; Publication No. US20050069869A1
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Search completed: June 30, 2005, 04:52:48  
Job time : 342.7 secs

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; GENERAL INFORMATION:
; APPLICANT: AMBROSINO, Donna
; APPLICANT: HERNANDEZ, Hector
; APPLICANT: GREENOUGH, Thomas
; APPLICANT: LUZURIAGA, Katherine
; APPLICANT: SOMASUNDARAN, Mohan
; APPLICANT: BABCOCK, Gregory J.
; APPLICANT: THOMAS, JR., William D.
; APPLICANT: SULLIVAN, John
; TITLE OF INVENTION: SARS NUCLEIC ACIDS, PROTEINS, ANTIBODIES
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: MJI-002
; CURRENT APPLICATION NUMBER: US/10/911,838
; CURRENT FILING DATE: 2004-08-04
; PRIOR APPLICATION NUMBER: US 60/565595
; PRIOR FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: US 60/545670
; PRIOR FILING DATE: 2004-02-18
; PRIOR APPLICATION NUMBER: US 60/510251
; PRIOR FILING DATE: 2003-10-09
; PRIOR APPLICATION NUMBER: US 60/492529
; PRIOR FILING DATE: 2003-08-04
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 81
; LENGTH: 70
; TYPE: DNA
; ORGANISM: SARS-Associated Coronavirus
US-10-911-838-81

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Query Match 26.7%; Score 16; DB 21; Length 70;  
Best Local Similarity 100.0%; Pred.No. 36;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 2 GTTCAACGGCACCTCC 17
Db 35 GTTCAACGGCACCTCC 20

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RESULT 15
US-09-560-863-437/c
; Sequence 437, Application US/09560863
; Patent No. US20020110809A1
; GENERAL INFORMATION:
; APPLICANT: Nehls, Michael C.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. US20020110809A1el Human Polynucleotides and the
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: LEX-0018-USA
; CURRENT APPLICATION NUMBER: US/09/560,863
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/132,408
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 1008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 437
; LENGTH: 406
; TYPE: DNA
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(406)
; OTHER INFORMATION: n = A,T,C or G
US-09-560-863-437

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Query Match 26.7%; Score 16; DB 9; Length 406;  
Best Local Similarity 100.0%; Pred.No. 29;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 2 GTTCAACGGCACCTCC 17
Db 208 GTTCAACGGCACCTCC 193

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 29, 2005, 19:26:35 ; Search time 51.2 Seconds  
(without alignments)  
1917.512 Million cell updates/sec

Title: US-10-057-136-12

Perfect score: 60  
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Scoring table: ~~omniscan~~  
Gapop 60.0 , Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq.\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq.\*  
5: /cgn2\_6/ptodata/1/ina/PTBUS\_COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/backfiles.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17	28.3	2208	4	US-09-489-039A-2376 Sequence 2376, Ap
2	16	26.7	240	4	US-09-252-991A-9393 Sequence 9393, Ap
3	16	26.7	837	4	US-09-252-991A-9468 Sequence 9468, Ap
4	16	26.7	1005	4	US-09-976-594-209 Sequence 209, App
5	16	26.7	1371	4	US-09-252-991A-9440 Sequence 9440, App
6	16	26.7	36075	4	US-09-949-016-16571 Sequence 16571, A
7	16	26.7	36075	4	US-09-949-016-16572 Sequence 16572, A
8	16	26.7	36625	4	US-09-949-016-12788 Sequence 12788, A
9	16	26.7	37133	4	US-09-949-016-16569 Sequence 16569, A
10	16	26.7	37133	4	US-09-949-016-16570 Sequence 16570, A
11	15	25.0	318	3	US-09-060-756-171 Sequence 171, App
12	15	25.0	318	4	US-09-670-314-171 Sequence 171, App
13	15	25.0	350	3	US-09-060-756-397 Sequence 397, App
14	15	25.0	350	4	US-09-670-314-397 Sequence 397, App
15	15	25.0	357	3	US-09-060-756-137 Sequence 137, App
16	15	25.0	357	4	US-09-670-314-137 Sequence 137, App
17	15	25.0	448	3	US-09-060-756-64 Sequence 64, Appl
18	15	25.0	448	4	US-09-670-314-64 Sequence 64, Appl
19	15	25.0	465	4	US-09-270-767-9372 Sequence 9372, Ap
20	15	25.0	465	4	US-09-270-767-24654 Sequence 24654, A
21	15	25.0	639	4	US-09-252-991A-14012 Sequence 14012, A
22	15	25.0	678	4	US-09-252-991A-14466 Sequence 14466, A
23	15	25.0	999	3	US-08-818-112-52 Sequence 52, Appl
24	15	25.0	999	3	US-08-818-111-52 Sequence 52, Appl
25	15	25.0	999	3	US-09-056-556-52 Sequence 52, Appl
26	15	25.0	999	3	US-09-072-967-52 Sequence 52, Appl
27	15	25.0	999	4	US-09-072-967-52 Sequence 52, Appl

28	15	25.0	1122	4	US-09-510-031A-1	Sequence 1, Appli
29	15	25.0	1269	4	US-09-252-991A-14054	Sequence 14054, A
c 30	15	25.0	1323	4	US-09-252-991A-14169	Sequence 14169, A
31	15	25.0	1374	4	US-09-252-991A-15159	Sequence 15159, A
c 32	15	25.0	1656	4	US-09-902-540-6531	Sequence 6531, Ap
33	15	25.0	1782	4	US-09-252-991A-14102	Sequence 14102, A
c 34	15	25.0	1872	4	US-09-252-991A-14602	Sequence 14602, A
35	15	25.0	1896	3	US-09-232-200-31	Sequence 31, Appl
36	15	25.0	1896	3	US-09-232-197-31	Sequence 31, Appl
37	15	25.0	1896	3	US-09-232-201-31	Sequence 31, Appl
38	15	25.0	1896	3	US-09-232-195-31	Sequence 31, Appl
39	15	25.0	1962	3	US-09-072-596-349	Sequence 349, App
40	15	25.0	1962	4	US-09-072-967-354	Sequence 354, App
41	15	25.0	2061	1	US-08-382-184-1	Sequence 1, Appli
42	15	25.0	2061	2	US-08-641-356-1	Sequence 1, Appli
43	15	25.0	2061	3	US-09-132-528-1	Sequence 1, Appli
44	15	25.0	2061	3	US-08-875-494-1	Sequence 1, Appli
45	15	25.0	2061	3	US-09-599-366-1	Sequence 1, Appli

## ALIGNMENTS

RESULT 1  
US-09-489-039A-2376  
; Sequence 2376, Application US/09489039A  
; Patent No. 6610836  
; GENERAL INFORMATION:  
; APPLICANT: Gary Breton et. al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
; FILE REFERENCE: 2709.2004001  
; CURRENT APPLICATION NUMBER: US/09/489,039A  
; CURRENT FILING DATE: 2000-01-27  
; PRIOR FILING DATE: US 60/117,747  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 14342  
; SEQ ID NO 2376  
; LENGTH: 2208  
; TYPE: DNA  
; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-2376

Query Match 28.3%; Score 17; DB 4; Length 2208;  
Best Local Similarity 100.0%; Pred. No. 3.6;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	4	AGTACAGCGCCACCGC	20
Db	2051	AGTACAGCGCCACCGC	2057

RESULT 2  
US-09-252-991A-9393  
; Sequence 9393, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR FILING DATE: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 9393  
; LENGTH: 240  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-9393

Query Match 26.7%; Score 16; DB 4; Length 240;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 CGAGCGCTCCGATAC 47  
Db 122 CGAGCGCTCCGATAC 137  
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RESULT 3  
US-09-252-991A-9468/c  
; Sequence 9468, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 9468  
; LENGTH: 837  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-9468

Query Match 26.7%; Score 16; DB 4; Length 837;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 CGAGCGCTCCGATAC 47  
Db 712 CGAGCGCTCCGATAC 697  
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RESULT 4  
US-09-976-594-209  
; Sequence 209, Application US/09976594  
; Patent No. 6673549  
; GENERAL INFORMATION:  
; APPLICANT: Furness, Michael  
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS  
; FILE REFERENCE: PA-0041 US  
; CURRENT APPLICATION NUMBER: US/09/976,594  
; CURRENT FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: 60/240,409  
; PRIOR FILING DATE: 2000-10-12  
; NUMBER OF SEQ ID NOS: 1143  
; SOFTWARE: PERL Program  
; SEQ ID NO 209  
; LENGTH: 1005  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; OTHER INFORMATION: Incyte ID No. 6673549 221433.21  
US-09-976-594-209

Query Match 26.7%; Score 16; DB 4; Length 1005;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CAGCGCCACCCGACCA 23  
Db 22 CAGCGCCACCCGACCA 37  
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RESULT 5  
US-09-252-991A-9440/c  
; Sequence 9440, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 9440  
; LENGTH: 1371  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-9440

Query Match 26.7%; Score 16; DB 4; Length 1371;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 CGAGCGCTCCGATAC 47  
Db 164 CGAGCGCTCCGATAC 149  
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RESULT 6  
US-09-949-016-16571  
; Sequence 16571, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 16571  
; LENGTH: 36075  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-16571

Query Match 26.7%; Score 16; DB 4; Length 36075;  
Best Local Similarity 100.0%; Pred. No. 9.8;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 CACCGCCACATGGCGT 29  
Db 25866 CACCGCCACATGGCGT 25881  
|||||

RESULT 7  
US-09-949-016-16572  
; Sequence 16572, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

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; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16572
; LENGTH: 36075
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16572

Query Match          26.7%; Score 16; DB 4; Length 36075;
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      14 CACCGGCACATGGCGT 29
Db      25866 CACCGGCACATGGCGT 25881

RESULT 8
US-09-949-016-12788
; Sequence 12788, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12788
; LENGTH: 36625
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12788

Query Match          26.7%; Score 16; DB 4; Length 36625;
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      14 CACCGGCACATGGCGT 29
Db      25866 CACCGGCACATGGCGT 25881

RESULT 9
US-09-949-016-16569
; Sequence 16569, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
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; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16569
; LENGTH: 37133
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16569

Query Match          26.7%; Score 16; DB 4; Length 37133;
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      14 CACCGGCACATGGCGT 29
Db      25866 CACCGGCACATGGCGT 25881

RESULT 10
US-09-949-016-16570
; Sequence 16570, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16570
; LENGTH: 37133
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16570

Query Match          26.7%; Score 16; DB 4; Length 37133;
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      14 CACCGGCACATGGCGT 29
Db      25866 CACCGGCACATGGCGT 25881

RESULT 11
US-09-060-756-171/c
; Sequence 171, Application US/09060756
; Patent No. 6183957
; GENERAL INFORMATION:
; APPLICANT: Cole, Stewart
; APPLICANT: Buchrieser-Brosch, Roland
; APPLICANT: Gordon, Stephen
; APPLICANT: Billault, Alain
; TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM
; TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA
; TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA
; FILE REFERENCE: 3495-0169
; CURRENT APPLICATION NUMBER: US/09/060,756
; CURRENT FILING DATE: 1998-04-16
; NUMBER OF SEQ ID NOS: 743
; SOFTWARE: Patent In Ver. 2.0
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; SEQ ID NO 171
; LENGTH: 318
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (various positions within the sequence)
; OTHER INFORMATION: applicants are uncertain of bases designated as "n"
US-09-060-756-171

Query Match      25.0%; Score 15; DB 3; Length 318;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      8 CAGCGCCACCCGCAC 22
Db      316 CAGCGCCACCCGCAC 302

RESULT 12
US-09-670-314-171/c
; Sequence 171, Application US/09670314
; Patent No. 6492506
; GENERAL INFORMATION:
; APPLICANT: Cole, Stewart
; APPLICANT: Buchrieser-Brosch, Roland
; APPLICANT: Gordon, Stephen
; APPLICANT: Billault, Alain
; TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM
; TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA
; TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA
; FILE REFERENCE: 3495-0169
; CURRENT APPLICATION NUMBER: US/09/670,314
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/060,756
; PRIOR FILING DATE: 1998-04-16
; NUMBER OF SEQ ID NOS: 743
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 171
; LENGTH: 318
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (various positions within the sequence)
; OTHER INFORMATION: applicants are uncertain of bases designated as "n"
US-09-670-314-171

Query Match      25.0%; Score 15; DB 4; Length 318;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      8 CAGCGCCACCCGCAC 22
Db      316 CAGCGCCACCCGCAC 302

RESULT 13
US-09-060-756-397/c
; Sequence 397, Application US/09060756
; Patent No. 6183957
; GENERAL INFORMATION:
; APPLICANT: Cole, Stewart
; APPLICANT: Buchrieser-Brosch, Roland
; APPLICANT: Gordon, Stephen
; APPLICANT: Billault, Alain
; TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM
; TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA
; TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA
; FILE REFERENCE: 3495-0169
; CURRENT APPLICATION NUMBER: US/09/060,756
; CURRENT FILING DATE: 1998-04-16
; NUMBER OF SEQ ID NOS: 743
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 397
; LENGTH: 350
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (various positions within the sequence)
; OTHER INFORMATION: applicants are uncertain of bases designated as "n"
US-09-060-756-397

Query Match      25.0%; Score 15; DB 3; Length 350;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      8 CAGCGCCACCCGCAC 22
Db      349 CAGCGCCACCCGCAC 335

RESULT 14
US-09-670-314-397/c
; Sequence 397, Application US/09670314
; Patent No. 6492506
; GENERAL INFORMATION:
; APPLICANT: Cole, Stewart
; APPLICANT: Buchrieser-Brosch, Roland
; APPLICANT: Gordon, Stephen
; APPLICANT: Billault, Alain
; TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM
; TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA
; TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA
; FILE REFERENCE: 3495-0169
; CURRENT APPLICATION NUMBER: US/09/670,314
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/060,756
; PRIOR FILING DATE: 1998-04-16
; NUMBER OF SEQ ID NOS: 743
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 397
; LENGTH: 350
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (various positions within the sequence)
; OTHER INFORMATION: applicants are uncertain of bases designated as "n"
US-09-670-314-397

Query Match      25.0%; Score 15; DB 4; Length 350;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      8 CAGCGCCACCCGCAC 22
Db      349 CAGCGCCACCCGCAC 335

RESULT 15
US-09-060-756-137/c
; Sequence 137, Application US/09060756
; Patent No. 6183957
; GENERAL INFORMATION:
; APPLICANT: Cole, Stewart
; APPLICANT: Buchrieser-Brosch, Roland
; APPLICANT: Gordon, Stephen
; APPLICANT: Billault, Alain
; TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM
; TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA
; TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA
; FILE REFERENCE: 3495-0169
; CURRENT APPLICATION NUMBER: US/09/060,756
; CURRENT FILING DATE: 1998-04-16
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; NUMBER OF SEQ ID NOS: 743
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 137
; LENGTH: 357
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-09-060-756-137
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Query Match      25.0%; Score 15; DB 3; Length 357;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      8 CAGCGCCACCCGCAC 22
      |||||
Db      353 CAGCGCCACCCGCAC 339
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Search completed: June 30, 2005, 04:10:29
Job time : 118.2 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

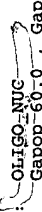
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Title: US-10-057-136-12

Perfect score: 60

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Gapop-60-0, Gapext 60.0

Searched: 6067389 seqs, 3125258755 residues

Word size : 0

Total number of hits satisfying chosen parameters: 12134778

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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- 9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*
- 10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*
- 12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*
- 13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*
- 14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*
- 15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*
- 16: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq:\*
- 17: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq:\*
- 18: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq:\*
- 19: /cgn2\_6/ptodata/1/pubpna/US10G\_PUBCOMB.seq:\*
- 20: /cgn2\_6/ptodata/1/pubpna/US10H\_PUBCOMB.seq:\*
- 21: /cgn2\_6/ptodata/1/pubpna/US10I\_PUBCOMB.seq:\*
- 22: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*
- 23: /cgn2\_6/ptodata/1/pubpna/US11A\_PUBCOMB.seq:\*
- 24: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq:\*
- 25: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*
- 26: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	60	100.0	60	14	US-10-057-136-12
2	60	100.0	2297	17	US-10-406-317-41
3	17	28.3	479	20	US-10-425-115-81989
4	17	28.3	1593	15	US-10-156-761-7089
5	17	28.3	2175	17	US-10-282-122A-23932
6	17	28.3	9025608	15	US-10-156-761-1
7	16	26.7	464	18	US-10-424-599-80160

Query Match 100.0%; Score 60; DB 14; Length 60;

c	8	16	26.7	565	19	US-10-437-963-60711	Sequence 60711, A
c	9	16	26.7	592	18	US-10-240-423-1352	Sequence 1352, Ap
c	10	16	26.7	1254	17	US-10-369-493-41496	Sequence 41496, A
c	11	16	26.7	1560	15	US-10-156-761-3612	Sequence 3612, Ap
c	12	16	26.7	1804	20	US-10-723-860-8253	Sequence 8253, Ap
c	13	16	26.7	2342	17	US-10-282-122A-23789	Sequence 23789, A
c	14	16	26.7	3708	17	US-10-282-122A-24775	Sequence 24775, A
c	15	16	26.7	32204	9	US-09-764-855-327	Sequence 327, App
c	16	16	26.7	32204	10	US-09-764-872-517	Sequence 517, App
c	17	16	26.7	32204	14	US-10-072-349-327	Sequence 327, App
c	18	16	26.7	9025608	15	US-10-156-761-1	Sequence 171, Appl
c	19	15	25.0	318	16	US-10-259-678-171	Sequence 171, Appl
c	20	15	25.0	350	16	US-10-259-678-397	Sequence 397, App
c	21	15	25.0	357	16	US-10-259-678-137	Sequence 137, App
c	22	15	25.0	384	11	US-09-864-408A-8011	Sequence 8011, Ap
c	23	15	25.0	424	20	US-10-425-115-168534	Sequence 168534, A
c	24	15	25.0	448	16	US-10-259-678-64	Sequence 64, Appl
c	25	15	25.0	472	20	US-10-425-115-20315	Sequence 20315, A
c	26	15	25.0	510	19	US-10-767-701-26375	Sequence 26375, A
c	27	15	25.0	534	15	US-10-198-677-141	Sequence 141, App
c	28	15	25.0	537	15	US-10-198-677-143	Sequence 143, App
c	29	15	25.0	633	15	US-10-156-761-1896	Sequence 1896, Ap
c	30	15	25.0	695	18	US-10-424-599-81094	Sequence 81094, A
c	31	15	25.0	755	20	US-10-653-047-1635	Sequence 1635, Ap
c	32	15	25.0	798	20	US-10-425-115-168658	Sequence 168658, A
c	33	15	25.0	896	18	US-10-425-114-28350	Sequence 28350, A
c	34	15	25.0	999	11	US-09-886-349A-40	Sequence 40, Appl
c	35	15	25.0	999	15	US-10-193-002-52	Sequence 52, Appl
c	36	15	25.0	999	15	US-10-084-843-52	Sequence 52, Appl
c	37	15	25.0	999	16	US-10-098-732A-40	Sequence 40, Appl
c	38	15	25.0	1008	15	US-10-156-761-3554	Sequence 3554, Ap
c	39	15	25.0	1080	18	US-10-425-114-25072	Sequence 25072, A
c	40	15	25.0	1086	17	US-10-282-122A-26278	Sequence 26278, A
c	41	15	25.0	1089	17	US-10-282-122A-28323	Sequence 28323, A
c	42	15	25.0	1122	17	US-10-369-493-44243	Sequence 44243, A
c	43	15	25.0	1125	18	US-10-425-114-34515	Sequence 34515, A
c	44	15	25.0	1125	20	US-10-425-115-65655	Sequence 65655, A
c	45	15	25.0	1160	20	US-10-425-115-65685	Sequence 65685, A

#### ALIGNMENTS

RESULT 1  
US-10-057-136-12  
; Sequence 12, Application US/10057136  
; Publication No. US20030021770A1  
; GENERAL INFORMATION:  
; APPLICANT: SCHLOM, JEFFREY  
; APPLICANT: KANTOR, JUDITH  
; APPLICANT: KUFE, DONALD  
; APPLICANT: PANICALI, DENNIS  
; APPLICANT: GRITZ, LINDA  
; TITLE OF INVENTION: RECOMBINANT POX VIRUS FOR IMMUNIZATION AGAINST MUC1  
; TITLE OF INVENTION: TUMOR-ASSOCIATED ANTIGEN  
; FILE REFERENCE: 700953/47113C  
; CURRENT APPLICATION NUMBER: US/10/057,136  
; PRIOR FILING DATE: 2002-01-25  
; PRIOR APPLICATION NUMBER: 09/366,670  
; PRIOR FILING DATE: 1999-08-03  
; PRIOR APPLICATION NUMBER: PCT/US98/03693  
; PRIOR FILING DATE: 1998-02-24  
; PRIOR APPLICATION NUMBER: 60/038,253  
; PRIOR FILING DATE: 1997-02-24  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 12  
; LENGTH: 60  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-057-136-12

Best Local Similarity 100.0%; Pred. No. 1e-24;  
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTAGTACAGCGCCACCGGCATGGGCTCAGAGCGCTCCGGATACGAGACCGCGCCT 60  
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Db 1 GGTAGTACAGCGCCACCGGCATGGGCTCAGAGCGCTCCGGATACGAGACCGCGCCT 60

## RESULT 2

US-10-406-317-41  
; Sequence 41, Application US/10406317  
; Publication No. US20040019195A1  
; GENERAL INFORMATION:  
; APPLICANT: Schlom, Jeffrey;  
; APPLICANT: Hodge, James;  
; APPLICANT: Panicali, Dennis  
; TITLE OF INVENTION: A recombinant vector expressing multiple constitutulatory  
; TITLE OF INVENTION: molecules and uses thereof  
; FILE REFERENCE: 38163-0189  
; CURRENT APPLICATION NUMBER: US/10/406,317  
; CURRENT FILING DATE: 2003-04-04  
; PRIOR APPLICATION NUMBER: US/09/856,988  
; PRIOR FILING DATE: 2001-05-30  
; PRIOR APPLICATION NUMBER: PCT/US99/26866  
; PRIOR FILING DATE: 1999-11-12  
; PRIOR APPLICATION NUMBER: 60/111,582  
; PRIOR FILING DATE: 1998-12-09  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 41  
; LENGTH: 2297  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: VECTOR  
US-10-406-317-41

Query Match 100.0%; Score 60; DB 17; Length 2297;  
Best Local Similarity 100.0%; Pred. No. 5.8e-25;  
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTAGTACAGCGCCACCGGCATGGGCTCAGAGCGCTCCGGATACGAGACCGCGCCT 60  
|||||  
Db 886 GGTAGTACAGCGCCACCGGCATGGGCTCAGAGCGCTCCGGATACGAGACCGCGCCT 945

## RESULT 3

US-10-425-115-81989/c  
; Sequence 81989, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 81989  
; LENGTH: 479  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_174788C.1  
US-10-425-115-81989

Query Match 28.3%; Score 17; DB 20; Length 479;  
Best Local Similarity 100.0%; Pred. No. 5.5;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 CGCACATGGCGTCACGA 34  
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Db 320 CGCACATGGCGTCACGA 304

## RESULT 4

US-10-156-761-7089/c  
; Sequence 7089, Application US/10156761  
; Publication No. US20030119018A1  
; GENERAL INFORMATION:  
; APPLICANT: OMURA, SATOSHI  
; APPLICANT: IKEDA, HARUO  
; APPLICANT: ISHIKAWA, JUN  
; APPLICANT: HORIKAWA, HIROSHI  
; APPLICANT: SHIBA, TADAYOSHI  
; APPLICANT: SAKAKI, YOSHIYUKI  
; APPLICANT: HATTORI, MASAHIRA  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
; FILE REFERENCE: 249-262  
; CURRENT APPLICATION NUMBER: US/10/156,761  
; CURRENT FILING DATE: 2002-05-29  
; PRIOR APPLICATION NUMBER: JP 2001-204089  
; PRIOR FILING DATE: 2001-05-30  
; PRIOR APPLICATION NUMBER: JP 2001-272697  
; PRIOR FILING DATE: 2001-08-02  
; NUMBER OF SEQ ID NOS: 15109  
; SEQ ID NO 7089  
; LENGTH: 1593  
; TYPE: DNA  
; ORGANISM: Streptomyces avermitilis  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1593)  
US-10-156-761-7089

Query Match 28.3%; Score 17; DB 15; Length 1593;  
Best Local Similarity 100.0%; Pred. No. 4.6;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 CGTCACGAGCGCTCCGG 43  
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Db 63 CGTCACGAGCGCTCCGG 47

## RESULT 5

US-10-282-122A-23932  
; Sequence 23932, Application US/10282122A  
; Publication No. US20040029129A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Liangsu  
; APPLICANT: Zamudio, Carlos  
; APPLICANT: Malone, Cheryl  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari  
; APPLICANT: Zyskind, Judith  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John  
; APPLICANT: Carr, Grant  
; APPLICANT: Yamamoto, Robert  
; APPLICANT: Forsyth, R.  
; APPLICANT: Xu, H.  
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
; FILE REFERENCE: ELITRA.034A  
; CURRENT APPLICATION NUMBER: US/10/282,122A  
; CURRENT FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/230,335

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; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23932
; LENGTH: 2175
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-10-282-122A-23932

Query Match      28.3%; Score 17; DB 17; Length 2175;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 AGTACAGCGCCACCGCG 20
Db      2021 AGTACAGCGCCACCGCG 2037

RESULT 6
US-10-156-761-1/c
; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, NASHAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1

Query Match      28.3%; Score 17; DB 15; Length 9025608;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      27 CGTCACGAGCGCTCCGG 43
Db      8469210 CGTCACGAGCGCTCCGG 8469194

RESULT 7
US-10-424-599-80160/c

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; Sequence 80160, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 80160
; LENGTH: 464
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_433C.1
US-10-424-599-80160

Query Match      26.7%; Score 16; DB 18; Length 464;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      42 GGATACGAGACCGCG 57
Db      405 GGATACGAGACCGCG 390

RESULT 8
US-10-437-963-60711/c
; Sequence 60711, Application US/10437963
; Publication No. US2004012343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 60711
; LENGTH: 565
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(565)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_62213C.1
US-10-437-963-60711

Query Match      26.7%; Score 16; DB 19; Length 565;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      16 CCCGACATGCGTCA 31
Db      191 CCCGACATGCGTCA 176

RESULT 9
US-10-240-425-1352
; Sequence 1352, Application US/10240425

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Publication No. US20040033502A1  
GENERAL INFORMATION:  
APPLICANT: Williams, Amanda  
APPLICANT: Boland, Joseph F.  
APPLICANT: Lord, Reginald V.  
APPLICANT: Alvarez, Chris  
APPLICANT: Wetzel, Jon C.  
APPLICANT: Scherf, Uwe  
APPLICANT: Vockley, Joseph G.  
TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue  
FILE REFERENCE: 44921-5026  
CURRENT APPLICATION NUMBER: US/10/240,425  
PRIOR FILING DATE: 2002-09-30  
PRIOR APPLICATION NUMBER: PCT/US01/09847  
PRIOR FILING DATE: 2001-03-28  
PRIOR APPLICATION NUMBER: US 60/193,446  
PRIOR FILING DATE: 2000-03-31  
NUMBER OF SEQ ID NOS: 1598  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO 1352  
LENGTH: 592  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
FEATURE:  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (1)..(592)  
OTHER INFORMATION: n = a or c or g or t  
US-10-240-425-1352

Query Match 26.7%; Score 16; DB 18; Length 592;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CAGCGCCACCCGCACA 23  
|||||  
Db 20 CAGCGCCACCCGCACA 35

## RESULT 10

US-10-369-493-41496/c  
Sequence 41496, Application US/10369493  
Publication No. US20030233675A1  
GENERAL INFORMATION:  
APPLICANT: Cao, Yongwei  
APPLICANT: Hinkle, Gregory J.  
APPLICANT: Slater, Steven C.  
APPLICANT: Goldman, Barry S.  
APPLICANT: Chen, Xianfeng  
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES  
FILE REFERENCE: 38-10(52052)B  
CURRENT APPLICATION NUMBER: US/10/369,493  
CURRENT FILING DATE: 2003-02-28  
PRIOR APPLICATION NUMBER: US 60/360,039  
PRIOR FILING DATE: 2002-02-21  
NUMBER OF SEQ ID NOS: 47374  
SEQ ID NO 41496  
LENGTH: 1254  
TYPE: DNA  
ORGANISM: SPHINGOMONAS  
US-10-369-493-41496

Query Match 26.7%; Score 16; DB 17; Length 1254;  
Best Local Similarity 100.0%; Pred. No. 18;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GTACAGCGCCACCCGC 20  
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Db 954 GTACAGCGCCACCCGC 939

## RESULT 11

US-10-156-761-3612/c  
Sequence 3612, Application US/10156761  
Publication No. US20030119018A1  
GENERAL INFORMATION:  
APPLICANT: OMURA, SATOSHI  
APPLICANT: IKEDA, HARUO  
APPLICANT: ISHIKAWA, JUN  
APPLICANT: HORIKAWA, HIROSHI  
APPLICANT: SHIBA, TADAYOSHI  
APPLICANT: SAKAKI, YOSHIYUKI  
APPLICANT: HATTORI, MASAHIRA  
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
FILE REFERENCE: 249-262  
CURRENT APPLICATION NUMBER: US/10/156,761  
CURRENT FILING DATE: 2002-05-29  
PRIOR APPLICATION NUMBER: JP 2001-204089  
PRIOR FILING DATE: 2001-05-30  
PRIOR APPLICATION NUMBER: JP 2001-272697  
PRIOR FILING DATE: 2001-08-02  
NUMBER OF SEQ ID NOS: 15109  
SEQ ID NO 3612  
LENGTH: 1560  
TYPE: DNA  
ORGANISM: Streptomyces avermitilis  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(1560)  
US-10-156-761-3612

Query Match 26.7%; Score 16; DB 15; Length 1560;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 CGCCACCCGCACATGG 26  
|||||  
Db 75 CGCCACCCGCACATGG 60

## RESULT 12

US-10-723-860-8253  
Sequence 8253, Application US/10723860  
Publication No. US20040253606A1  
GENERAL INFORMATION:  
APPLICANT: Aziz, Natasha  
APPLICANT: Ginsburg, Wendy M.  
APPLICANT: Zlotnik, Albert  
TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &  
TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators  
FILE REFERENCE: 05882, 0193.NPUS01  
CURRENT APPLICATION NUMBER: US/10/723,860  
CURRENT FILING DATE: 2003-11-26  
PRIOR APPLICATION NUMBER: 60/429,739  
PRIOR FILING DATE: 2002-11-26  
NUMBER OF SEQ ID NOS: 8393  
SOFTWARE: Patent in version 3.2  
SEQ ID NO 8253  
LENGTH: 1804  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-723-860-8253

Query Match 26.7%; Score 16; DB 20; Length 1804;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CAGCGCCACCCGCACA 23  
|||||  
Db 307 CAGCGCCACCCGCACA 322

## RESULT 13

US-10-282-122A-31789/c



---



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 29, 2005, 19:26:35 ; Search time 51.2 Seconds  
(without alignments)  
1917.512 Million cell updates/sec

Title: US-10-057-136-2

Perfect score: 60

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Scoring table: ~~WILCOX~~

Gapop 60.0 , Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents NA.\*

- 1: /cgn2\_6/ptodata/1/ina/5A COMB.seq.\*
- 2: /cgn2\_6/ptodata/1/ina/5B COMB.seq.\*
- 3: /cgn2\_6/ptodata/1/ina/6A COMB.seq.\*
- 4: /cgn2\_6/ptodata/1/ina/6B COMB.seq.\*
- 5: /cgn2\_6/ptodata/1/ina/PCTUS COMB.seq.\*
- 6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	60	100.0	1804	US-10-029-517-17	Sequence 17, Appl
2	60	100.0	8186	US-10-029-517-19	Sequence 19, Appl
3	57	95.0	518	US-10-029-517-101	Sequence 101, Appl
4	54	90.0	60	US-09-475-947A-246	Sequence 246, Appl
5	54	90.0	1721	US-10-029-517-3	Sequence 3, Appl
6	43	71.7	572	US-10-029-517-18	Sequence 18, Appl
7	27	45.0	6192	US-08-479-537A-1	Sequence 1, Appl
8	27	45.0	6192	US-09-083-116-1	Sequence 1, Appl
9	27	45.0	6192	US-09-134-916A-1	Sequence 1, Appl
10	27	45.0	6449	US-08-479-537A-4	Sequence 4, Appl
11	27	45.0	6449	US-09-083-116-4	Sequence 4, Appl
12	27	45.0	6449	US-09-134-916A-4	Sequence 4, Appl
13	23	38.3	981	US-10-029-517-16	Sequence 16, Appl
14	23	38.3	3343	US-10-029-517-102	Sequence 102, Appl
15	17	28.3	2001	US-09-489-039A-3650	Sequence 3650, App
16	17	28.3	2145	US-09-489-039A-3938	Sequence 3938, Ap
17	17	28.3	14516	US-09-949-016-17047	Sequence 17047, A
18	16	26.7	601	US-09-949-016-21132	Sequence 21132, A
19	16	26.7	601	US-09-949-016-21133	Sequence 21133, A
20	16	26.7	601	US-09-949-016-21134	Sequence 21134, A
21	16	26.7	601	US-09-949-016-36255	Sequence 36255, A
22	16	26.7	601	US-09-949-016-47500	Sequence 47500, A
23	16	26.7	601	US-09-949-016-47501	Sequence 47501, A
24	16	26.7	601	US-09-949-016-47502	Sequence 47502, A
25	16	26.7	601	US-09-949-016-51958	Sequence 51958, A
26	16	26.7	927	US-09-804-778A-1	Sequence 1, Appl
27	16	26.7	1431	US-09-252-991A-2821	Sequence 2821, Ap

#### ALIGNMENTS

##### RESULT 1

US-10-029-517-17  
; Sequence 17, Application US/10029517  
; Patent No. 6716627  
; GENERAL INFORMATION:  
; APPLICANT: Kenneth W. Dobie  
; APPLICANT: Susan J. Myers  
; TITLE OF INVENTION: ANTISENSE MODULATION OF MUCIN 1, TRANSMEMBRANE EXPRESSION  
; FILE REFERENCE: RIS-0352  
; CURRENT APPLICATION NUMBER: US/10/029,517  
; CURRENT FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 107  
; SEQ ID NO 17  
; LENGTH: 1804  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (73)...(1500)  
US-10-029-517-17

Query Match 100.0%; Score 60; DB 4; Length 1804;  
Best Local Similarity 100.0%; Pred.No. 1e-20;  
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGCTCCACCGCCCCCCCCAGCCCGGTGTACCTCGGCGCCGACACCGCCGCCCCG 60  
Db 457 GGCTCCACCGCCCCCCCCAGCCCGGTGTACCTCGGCGCCGACACCGCCGCCCCG 516

##### RESULT 2

US-10-029-517-19  
; Sequence 19, Application US/10029517  
; Patent No. 6716627  
; GENERAL INFORMATION:  
; APPLICANT: Kenneth W. Dobie  
; APPLICANT: Susan J. Myers  
; TITLE OF INVENTION: ANTISENSE MODULATION OF MUCIN 1, TRANSMEMBRANE EXPRESSION  
; FILE REFERENCE: RIS-0352  
; CURRENT APPLICATION NUMBER: US/10/029,517  
; CURRENT FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 107  
; SEQ ID NO 19  
; LENGTH: 8186  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: 6899  
; OTHER INFORMATION: unknown  
US-10-029-517-19

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; NAME/KEY: unsure
; LOCATION: 7155
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 7184
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 7957
; OTHER INFORMATION: unknown
; NAME/KEY: intron
; LOCATION: (2997)...(3498)
; OTHER INFORMATION: intron 1
; NAME/KEY: intron:exon junction
; LOCATION: (3498)...(3499)
; OTHER INFORMATION: intron 1:exon 2
; NAME/KEY: exon
; LOCATION: (3508)...(3599)
; OTHER INFORMATION: exon 2d
; NAME/KEY: exon:intron junction
; LOCATION: (3982)...(3983)
; OTHER INFORMATION: exon 2a:intron 2a
; NAME/KEY: intron:exon junction
; LOCATION: (4205)...(4206)
; OTHER INFORMATION: intron 2c:exon 3c
; NAME/KEY: intron:exon junction
; LOCATION: (4259)...(4260)
; OTHER INFORMATION: intron 2d:exon 3d
; NAME/KEY: exon
; LOCATION: (4260)...(4328)
; OTHER INFORMATION: exon 3d
; NAME/KEY: intron:exon junction
; LOCATION: (4632)...(4633)
; OTHER INFORMATION: intron 3:exon 4
; NAME/KEY: exon
; LOCATION: (4914)...(5035)
; OTHER INFORMATION: exon 5
; NAME/KEY: intron
; LOCATION: (5266)...(6293)
; OTHER INFORMATION: intron 6
US-10-029-517-19

Query Match 100.0%; Score 60; DB 4; Length 8186;
Best Local Similarity 100.0%; Pred. No. 8.8e-21;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCTCCACCGCCCCCGCCAGCCAGCGGTGTCACTCGGCCCGCGGACACCCAGCGCGCCCG 60
Db 3825 GGCTCCACCGCCCCCGCCAGCCAGCGGTGTCACTCGGCCCGCGGACACCCAGCGCGCCCG 3884

RESULT 3
US-10-029-517-101
; Sequence 101, Application US/10029517
; Patent No. 6716627
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; APPLICANT: Susan J. Myers
; TITLE OF INVENTION: ANTISENSE MODULATION OF MUCIN 1, TRANSMEMBRANE EXPRESSION
; FILE REFERENCE: RTS-0352
; CURRENT APPLICATION NUMBER: US/10/029,517
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 107
; SEQ ID NO 101
; LENGTH: 518
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-10-029-517-101

Query Match 95.0%; Score 57; DB 4; Length 518;
Best Local Similarity 100.0%; Pred. No. 3.4e-19;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 GGCTCCACCGCCCCCGCCAGCCAGCGGTGTCACTCGGCCCGCGGACACCCAGCGCGCC 57
Db 462 GGCTCCACCGCCCCCGCCAGCCAGCGGTGTCACTCGGCCCGCGGACACCCAGCGCGCC 518

RESULT 4
US-09-475-947A-246
; Sequence 246, Application US/09475947A
; Patent No. 6472154
; GENERAL INFORMATION:
; APPLICANT: Garner, Harold R.
; APPLICANT: Wren, Jonathan D.
; APPLICANT: Minna, John D.
; TITLE OF INVENTION: Polymorphic Repeats in Human Genes
; FILE REFERENCE: UTS00667
; CURRENT APPLICATION NUMBER: US/09/475,947A
; CURRENT FILING DATE: 1999-12-31
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 246
; LENGTH: 60
; TYPE: DNA
; ORGANISM: human
US-09-475-947A-246

Query Match 90.0%; Score 54; DB 4; Length 60;
Best Local Similarity 100.0%; Pred. No. 1.3e-17;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCTCCACCGCCCCCGCCAGCCAGCGGTGTCACTCGGCCCGCGGACACCCAGCGCG 54
Db 7 GGCTCCACCGCCCCCGCCAGCCAGCGGTGTCACTCGGCCCGCGGACACCCAGCGCG 60

RESULT 5
US-10-029-517-3
; Sequence 3, Application US/10029517
; Patent No. 6716627
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; APPLICANT: Susan J. Myers
; TITLE OF INVENTION: ANTISENSE MODULATION OF MUCIN 1, TRANSMEMBRANE EXPRESSION
; FILE REFERENCE: RTS-0352
; CURRENT APPLICATION NUMBER: US/10/029,517
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 107
; SEQ ID NO 3
; LENGTH: 1721
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (58)...(1605)
US-10-029-517-3

Query Match 90.0%; Score 54; DB 4; Length 1721;
Best Local Similarity 100.0%; Pred. No. 9.3e-18;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCTCCACCGCCCCCGCCAGCCAGCGGTGTCACTCGGCCCGCGGACACCCAGCGCG 54
Db 442 GGCTCCACCGCCCCCGCCAGCCAGCGGTGTCACTCGGCCCGCGGACACCCAGCGCG 495

RESULT 6
US-10-029-517-18
; Sequence 18, Application US/10029517
; Patent No. 6716627
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; APPLICANT: Susan J. Myers
; TITLE OF INVENTION: ANTISENSE MODULATION OF MUCIN 1, TRANSMEMBRANE EXPRESSION
; FILE REFERENCE: RTS-0352
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; CURRENT APPLICATION NUMBER: US/10/029,517
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 107
; SEQ ID NO 18
; LENGTH: 572
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (67)...(572)
US-10-029-517-18

Query Match          71.7%; Score 43; DB 4; Length 572;
Best Local Similarity 100.0%; Pred. No. 2.8e-12;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 AGCCACGGTGTACCTCGGCCGGACACAGGCGGCCCG 60
Db 495 AGCCACGGTGTACCTCGGCCGGACACAGGCGGCCCG 537

RESULT 7
US-08-479-537A-1
; Sequence 1, Application US/08479537A
; Patent No. 5861381
; GENERAL INFORMATION:
; APPLICANT: CHAMBON, Pierre
; APPLICANT: KIENY, Marie-Paule
; APPLICANT: LATHE, Richard
; APPLICANT: HAREUVENI, Mara
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION FOR THE
; TITLE OF INVENTION: TREATMENT OR PREVENTION OF A MALIGNANT TUMOR
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,537A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 90/13101
; FILING DATE: 23-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR91/00835
; FILING DATE: 23-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/039,320
; FILING DATE: 04-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/403,576
; FILING DATE: 14-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 017753-025
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6192 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 58..120
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 439..5239
; OTHER INFORMATION: /note= "The nucleotides spanning
; OTHER INFORMATION: 439-5239 constitute a repeated region wherein the repeat is 6
; OTHER INFORMATION: nucleotides and encodes 20 amino acids, 17 of which are fixed
; OTHER INFORMATION: The number of such repeats varies from 1 to 80."
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 121..6166
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 457
; OTHER INFORMATION: /note= "Nucleotide 457 is X1 = NNN
; OTHER INFORMATION: which is the codon for Pro or Ala wherein Pro = CCT, CCC, CCA
; OTHER INFORMATION: or CCG; and Ala = GCT, GCC, GCA, or GCG."
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 487
; OTHER INFORMATION: /note= "Nucleotide 487 is Y = NNN
; OTHER INFORMATION: which is the codon for Thr or Asn wherein Thr = ACT, ACC, ACA
; OTHER INFORMATION: or ACG; and Asn = AAT or AAC."
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 496
; OTHER INFORMATION: /note= "Nucleotide 496 is X2 = NNN
; OTHER INFORMATION: which is the codon for Pro or Ala wherein Pro = CCT, CCC, CCA
; OTHER INFORMATION: or CCG; and Ala = GCT, GCC, GCA, or GCG."
US-08-479-537A-1

Query Match          45.0%; Score 27; DB 2; Length 6192;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 GCCCAGGTGTACCTCGGCCCGGAC 45
Db 460 GCCCAGGTGTACCTCGGCCCGGAC 486

RESULT 8
US-09-083-116-1
; Sequence 1, Application US/09083116
; Patent No. 6203795
; GENERAL INFORMATION:
; APPLICANT: CHAMBON, Pierre
; APPLICANT: KIENY, Marie-Paule
; APPLICANT: LATHE, Richard
; APPLICANT: HAREUVENI, Mara
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION FOR THE
; TITLE OF INVENTION: TREATMENT OR PREVENTION OF A MALIGNANT TUMOR
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/083,116
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: 08/479,537
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR91/00835
; FILING DATE: 23-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/039,320
; FILING DATE: 04-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/403,576
; FILING DATE: 14-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 017753-025
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6192 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 58..120
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 439..5239
; OTHER INFORMATION: /note= "The nucleotides spanning
; 439-5239 constitute a repeated region wherein the repeat is 6
; nucleotides and encodes 20 amino acids, 17 of which are fixed
; The number of such repeats varies from 1 to 80."
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 121..6166
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 457
; OTHER INFORMATION: /note= "Nucleotide 457 is X1 = NNN
; which is the codon for Pro or Ala wherein Pro = CCT, CCC, CCA
; or CCG; and Ala = GCT, GCC, GCA, or GCG."
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 487
; OTHER INFORMATION: /note= "Nucleotide 487 is Y = NNN
; which is the codon for Thr or Asn wherein Thr = ACT, ACC, ACA
; or ACG; and Asn = AAT or AAC."
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 496
; OTHER INFORMATION: /note= "Nucleotide 496 is X2 = NNN
; which is the codon for Pro or Ala wherein Pro = CCT, CCC, CCA
; or CCG; and Ala = GCT, GCC, GCA, or GCG."
;
; US-09-083-116-1
;
; Query Match 45.0%; Score 27; DB 3; Length 6192;
; Best Local Similarity 100.0%; Pred. No. 0.00018;
; Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; Qy 19 GCCCAGCGTGTCACTCGGCCCGGAC 45
;
; Db 460 GCCCAGCGTGTCACTCGGCCCGGAC 486
;
; RESULT 9
; US-09-134-916A-1
; Sequence 1, Application US/09134916A
; Patent No. 6328956
; GENERAL INFORMATION:
; APPLICANT: CHAMBON, Pierre
```

```
; APPLICANT: KIENY, Marie-Paule
; APPLICANT: LATHE, Richard
; APPLICANT: HAREUVENI, Mara
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION FOR THE
; TREATMENT OR PREVENTION OF A MALIGNANT TUMOR
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/134,916A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,537
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: FR 90/13101
; FILING DATE: 23-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR91/00835
; FILING DATE: 23-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/039,320
; FILING DATE: 04-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/403,576
; FILING DATE: 14-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 017753-025
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6192 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 58..120
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 439..5239
; OTHER INFORMATION: /note= "The nucleotides spanning
; 439-5239 constitute a repeated region wherein the repeat is 6
; nucleotides and encodes 20 amino acids, 17 of which are fixed
; The number of such repeats varies from 1 to 80."
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 121..6166
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 457
; OTHER INFORMATION: /note= "Nucleotide 457 is X1 = NNN
; which is the codon for Pro or Ala wherein Pro = CCT, CCC, CCA
; or CCG; and Ala = GCT, GCC, GCA, or GCG."
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 487
; OTHER INFORMATION: /note= "Nucleotide 487 is Y = NNN
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; OTHER INFORMATION: which is the codon for Thr or Asn wherein Thr = ACT, ACC, ACA
; OTHER INFORMATION: or ACG; and Asn = AAT or AAC."
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 496
; OTHER INFORMATION: /note= "Nucleotide 496 is X2 = NNN
; OTHER INFORMATION: which is the codon for Pro or Ala wherein Pro = CCT, CCC, CCA
; OTHER INFORMATION: or CCG; and Ala = GCT, GCC, GCA, or GCG."
US-09-134-916A-1

Query Match          45.0%; Score 27; DB 3; Length 6192;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 GCCCAGCGTGTCACCTCGGCCCGGAC 45
Db 460 GCCCAGCGTGTCACCTCGGCCCGGAC 486

RESULT 10
US-08-479-537A-4
; Sequence 4, Application US/08479537A
; Patent No. 5861381
; GENERAL INFORMATION:
; APPLICANT: CHAMBER, Pierre
; APPLICANT: KIENY, Marie-Paule
; APPLICANT: LATHE, Richard
; APPLICANT: HAREUVENI, Mara
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION FOR THE
; TITLE OF INVENTION: TREATMENT OR PREVENTION OF A MALIGNANT TUMOR
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,537A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 90/13101
; FILING DATE: 23-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR91/00835
; FILING DATE: 23-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/039,320
; FILING DATE: 04-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/403,576
; FILING DATE: 14-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 017753-025
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6449 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
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; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 58..120
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 439..5239
; OTHER INFORMATION: /note= "The nucleotides spanning
; OTHER INFORMATION: 439-5239 constitute a repeated region wherein the repeat is 6
; OTHER INFORMATION: nucleotides and encodes 20 amino acids, 17 of which are fixed
; OTHER INFORMATION: The number of such repeats varies from 1 to 80."
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 121..5661
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 457
; OTHER INFORMATION: /note= "Nucleotide 457 is X1 = NNN
; OTHER INFORMATION: which is the codon for Pro or Ala wherein Pro = CCT, CCC, CCA
; OTHER INFORMATION: or CCG; and Ala = GCT, GCC, GCA, or GCG."
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 487
; OTHER INFORMATION: /note= "Nucleotide 487 is Y = NNN
; OTHER INFORMATION: which is the codon for Thr or Asn wherein Thr = ACT, ACC, ACA
; OTHER INFORMATION: or ACG; and Asn = AAT or AAC."
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 496
; OTHER INFORMATION: /note= "Nucleotide 496 is X2 = NNN
; OTHER INFORMATION: which is the codon for Pro or Ala wherein Pro = CCT, CCC, CCA
; OTHER INFORMATION: or CCG; and Ala = GCT, GCC, GCA, or GCG."
US-08-479-537A-4

Query Match          45.0%; Score 27; DB 2; Length 6449;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 GCCCAGCGTGTCACCTCGGCCCGGAC 45
Db 460 GCCCAGCGTGTCACCTCGGCCCGGAC 486

RESULT 11
US-09-083-116-4
; Sequence 4, Application US/09083116
; Patent No. 6203795
; GENERAL INFORMATION:
; APPLICANT: CHAMBER, Pierre
; APPLICANT: KIENY, Marie-Paule
; APPLICANT: LATHE, Richard
; APPLICANT: HAREUVENI, Mara
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION FOR THE
; TITLE OF INVENTION: TREATMENT OR PREVENTION OF A MALIGNANT TUMOR
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/083,116
; FILING DATE: 08/09/083,116
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/479,537
; FILING DATE:
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR91/00835
; FILING DATE: 23-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/039,320
; FILING DATE: 04-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/403,576
; FILING DATE: 14-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 017753-025
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6449 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 58..120
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 439..5239
; OTHER INFORMATION: /note= "The nucleotides spanning
; OTHER INFORMATION: 439-5239 constitute a repeated region wherein the repeat is 6
; OTHER INFORMATION: nucleotides and encodes 20 amino acids, 17 of which are fixed
; OTHER INFORMATION: The number of such repeats varies from 1 to 80."
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 121..5661
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 457
; OTHER INFORMATION: /note= "Nucleotide 457 is X1 = NNN
; OTHER INFORMATION: which is the codon for Pro or Ala wherein Pro = CCT, ACC, ACA
; OTHER INFORMATION: or ACG; and Asn = AAT or AAC."
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 487
; OTHER INFORMATION: /note= "Nucleotide 487 is Y = NNN
; OTHER INFORMATION: which is the codon for Thr or Asn wherein Thr = ACT, ACC, ACA
; OTHER INFORMATION: or ACG; and Ala = GCT, GCC, GCA, or GCG."
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 496
; OTHER INFORMATION: /note= "Nucleotide 496 is X2 = NNN
; OTHER INFORMATION: which is the codon for Pro or Ala wherein Pro = CCT, CCC, CCA
; OTHER INFORMATION: or CCG; and Ala = GCT, GCC, GCA, or GCG."
;
; US-09-083-116-4
; Query Match 45.0%; Score 27; DB 3; Length 6449;
; Best Local Similarity 100.0%; Pred. No. 0.00018;
; Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; Qy 19 GCCACGGTGTCACTCGGCCCGGAC 45
; |||||
; Db 460 GCCACGGTGTCACTCGGCCCGGAC 486
;
; RESULT 12
; US-09-134-916A-4
; Sequence 4, Application US/09134916A
; Patent No. 6328956
; GENERAL INFORMATION:
; APPLICANT: CHAMBERON, Pierre
; APPLICANT: KIENY, Marie-Paule
; APPLICANT: LATHE, Richard
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; APPLICANT: HAREUUVENI, Mara
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION FOR THE
; TITLE OF INVENTION: TREATMENT OR PREVENTION OF A MALIGNANT TUMOR
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patencin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/134,916A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,537
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: FR 90/13101
; FILING DATE: 23-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR91/00835
; FILING DATE: 23-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/039,320
; FILING DATE: 04-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/403,576
; FILING DATE: 14-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 017753-025
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6449 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 58..120
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 439..5239
; OTHER INFORMATION: /note= "The nucleotides spanning
; OTHER INFORMATION: 439-5239 constitute a repeated region wherein the repeat is 6
; OTHER INFORMATION: nucleotides and encodes 20 amino acids, 17 of which are fixed
; OTHER INFORMATION: The number of such repeats varies from 1 to 80."
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 121..5661
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 457
; OTHER INFORMATION: /note= "Nucleotide 457 is X1 = NNN
; OTHER INFORMATION: which is the codon for Pro or Ala wherein Pro = CCT, CCC, CCA
; OTHER INFORMATION: or CCG; and Ala = GCT, GCC, GCA, or GCG."
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 487
; OTHER INFORMATION: /note= "Nucleotide 487 is Y = NNN
; OTHER INFORMATION: which is the codon for Thr or Asn wherein Thr = ACT, ACC, ACA
; OTHER INFORMATION: or ACG; and Asn = AAT or AAC."
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 496
; OTHER INFORMATION: /note= "Nucleotide 496 is X2 = NNN
; OTHER INFORMATION: which is the codon for Pro or Ala wherein Pro = CCT, CCC, CCA
; OTHER INFORMATION: or CCG; and Ala = GCT, GCC, GCA, or GCG."
;
; US-09-134-916A-4
; Sequence 4, Application US/09134916A
; Patent No. 6328956
; GENERAL INFORMATION:
; APPLICANT: CHAMBERON, Pierre
; APPLICANT: KIENY, Marie-Paule
; APPLICANT: LATHE, Richard
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; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 496
; OTHER INFORMATION: /note= "Nucleotide 496 is X2 = NNN
; OTHER INFORMATION: which is the codon for Pro or Ala wherein Pro = CCT, CCC, CCA
; OTHER INFORMATION: or CCG; and Ala = GCT, GCC, GCA, or GCG."
US-09-134-916A-4

Query Match          45.0%; Score 27; DB 3; Length 6449;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 GCCACGGTGTCACCTCGGCCCGGAC 45
Db 460 GCCACGGTGTCACCTCGGCCCGGAC 486

RESULT 13
US-10-029-517-16
; Sequence 16, Application US/10029517
; Patent No. 6716627
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF MUCIN 1, TRANSMEMBRANE EXPRESSION
; FILE REFERENCE: RTS-0352
; CURRENT APPLICATION NUMBER: US/10/029,517
; PRIOR FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 107
; SEQ ID NO 16
; LENGTH: 981
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: exon:exon junction
; LOCATION: (464)...(465)
; OTHER INFORMATION: exon 3b:exon 4
US-10-029-517-16

Query Match          38.3%; Score 23; DB 4; Length 981;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCTCCACCGCCCGCCCGCCAGCCCA 23
Db 21 GGCTCCACCGCCCGCCCGCCAGCCCA 43

RESULT 14
US-10-029-517-102
; Sequence 102, Application US/10029517
; Patent No. 6716627
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; APPLICANT: Susan J. Myers
; TITLE OF INVENTION: ANTISENSE MODULATION OF MUCIN 1, TRANSMEMBRANE EXPRESSION
; FILE REFERENCE: RTS-0352
; CURRENT APPLICATION NUMBER: US/10/029,517
; PRIOR FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 107
; SEQ ID NO 102
; LENGTH: 3343
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY:
US-10-029-517-102

Query Match          38.3%; Score 23; DB 4; Length 3343;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCTCCACCGCCCGCCCGCCAGCCCA 23
Db 21 GGCTCCACCGCCCGCCCGCCAGCCCA 43

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; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 1668
; OTHER INFORMATION: /note= "Nucleotide 1668 is X2 = NNN
; OTHER INFORMATION: which is the codon for Pro or Ala wherein Pro = CCT, CCC, CCA
; OTHER INFORMATION: or CCG; and Ala = GCT, GCC, GCA, or GCG."
US-09-039A-3650/c
; Sequence 3650, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709,2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 3650
; LENGTH: 2001
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-3650

Query Match          28.3%; Score 17; DB 4; Length 2001;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 37 GCCCGGACACCCAGGCC 53
Db 920 GCCCGGACACCCAGGCC 904

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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Title: US-10-057-136-2

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Gapop 60.0 , Gapext 60.0

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21:	/cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq.*
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24:	/cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
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C 3	60	100.0	1424	21	Sequence 75, Appl
4	60	100.0	1428	17	Sequence 75, Appl
5	60	100.0	1428	21	Sequence 20, Appl
6	60	100.0	1428	21	Sequence 20, Appl
7	60	100.0	1527	14	Sequence 19, Appl
	60	100.0	1799	17	Sequence 19, Appl

Query Match 100.0%; Score 60; DB 14; Length 60;

8	60	100.0	1799	21	US-10-778-859-19	Sequence 19, Appl
9	60	100.0	1804	9	US-09-964-824A-573	Sequence 573, Appl
10	60	100.0	1804	15	US-10-029-517-17	Sequence 17, Appl
11	60	100.0	1804	19	US-10-717-597-30	Sequence 30, Appl
12	60	100.0	1804	19	US-10-775-920-84	Sequence 84, Appl
13	60	100.0	1804	21	US-10-843-641A-5876	Sequence 5876, Ap
14	60	100.0	1823	15	US-10-101-510-339	Sequence 339, App
15	60	100.0	2297	17	US-10-406-317-41	Sequence 41, Appl
16	60	100.0	4139	9	US-09-964-824A-105	Sequence 105, App
17	60	100.0	4139	9	US-09-964-824A-578	Sequence 578, App
18	60	100.0	4139	9	US-09-864-864-334	Sequence 334, App
19	60	100.0	4139	9	US-09-880-107-2121	Sequence 2121, Ap
20	60	100.0	4139	11	US-09-968-007A-751	Sequence 751, App
21	60	100.0	4139	14	US-10-171-311-157	Sequence 157, App
22	60	100.0	4139	15	US-10-177-293-310	Sequence 310, App
23	60	100.0	4139	17	US-10-440-464-155	Sequence 155, App
24	60	100.0	4139	19	US-10-734-564-53	Sequence 53, Appl
25	60	100.0	4139	19	US-10-775-920-80	Sequence 80, Appl
26	60	100.0	4139	19	US-10-775-920-85	Sequence 85, Appl
27	60	100.0	4139	21	US-10-843-641A-5408	Sequence 5408, Ap
28	60	100.0	4139	21	US-10-843-641A-5881	Sequence 5881, Ap
29	60	100.0	4139	21	US-10-843-641A-7221	Sequence 7221, Ap
30	60	100.0	8181	11	US-09-951-938-18	Sequence 18, Appl
31	60	100.0	8181	17	US-10-447-839A-18	Sequence 18, Appl
32	60	100.0	8181	21	US-10-778-859-18	Sequence 18, Appl
33	60	100.0	8186	15	US-10-029-517-19	Sequence 19, Appl
34	60	100.0	8186	21	US-10-696-639-21	Sequence 21, Appl
35	57	95.0	518	15	US-10-029-517-101	Sequence 101, App
36	54	90.0	1721	9	US-09-864-864-280	Sequence 280, App
37	54	90.0	1721	9	US-09-967-768A-224	Sequence 224, App
38	54	90.0	1721	14	US-10-097-340-211	Sequence 211, App
39	54	90.0	1721	14	US-10-171-311-155	Sequence 155, App
40	54	90.0	1721	15	US-10-007-926A-58	Sequence 58, Appl
41	54	90.0	1721	15	US-10-029-517-3	Sequence 3, Appli
42	54	90.0	1721	17	US-10-172-118-775	Sequence 775, App
43	54	90.0	1721	18	US-10-342-887-775	Sequence 775, App
44	54	90.0	1721	19	US-10-775-920-88	Sequence 88, Appl
45	54	90.0	1721	21	US-10-843-641A-6369	Sequence 6369, Ap

#### ALIGNMENTS

RESULT 1  
US-10-057-136-2  
; Sequence 2, Application US/10057136  
; Publication No. US20030021770A1  
; GENERAL INFORMATION:  
; APPLICANT: SCHLOM, JEFFREY  
; APPLICANT: KANTOR, JUDITH  
; APPLICANT: KUFE, DONALD  
; APPLICANT: PANICALI, DENNIS  
; APPLICANT: GRITZ, LINDA  
; TITLE OF INVENTION: RECOMBINANT POX VIRUS FOR IMMUNIZATION AGAINST MUC1  
; FILE OF INVENTION: TUMOR-ASSOCIATED ANTIGEN  
; FILE REFERENCE: 700953/47113C  
; CURRENT APPLICATION NUMBER: US/10/057,136  
; CURRENT FILING DATE: 2002-01-25  
; PRIOR APPLICATION NUMBER: 09/366,670  
; PRIOR FILING DATE: 1999-08-03  
; PRIOR APPLICATION NUMBER: PCT/US98/03693  
; PRIOR FILING DATE: 1998-02-24  
; PRIOR APPLICATION NUMBER: 60/038,253  
; PRIOR FILING DATE: 1997-02-24  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: Patent Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 60  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-057-136-2

Best Local Similarity 100.0%; Pred. No. 3.7e-22;  
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGCTCCACCGCCCCCAGCCACGGTGTACCTCGGCCCGCGGACACACAGCGCGGCCCG 60  
Db 1 GGCTCCACCGCCCCCAGCCACGGTGTACCTCGGCCCGCGGACACACAGCGCGGCCCG 60

## RESULT 2

US-10-447-839A-75/c  
; Sequence 75, Application US/10447839A  
; Publication No. US20040018181A1  
; GENERAL INFORMATION:  
; APPLICANT: Kufe, Donald W.  
; APPLICANT: Kharbanda, Surender  
; APPLICANT: Weitman, Steven D.  
; TITLE OF INVENTION: MUC1 INTERFERENCE RNA COMPOSITIONS AND METHODS DERIVED THEREFROM  
; FILE REFERENCE: 1000.05.009  
; CURRENT APPLICATION NUMBER: US/10/447,839A  
; CURRENT FILING DATE: 2003-05-29  
; PRIOR APPLICATION NUMBER: 10/293,391  
; PRIOR FILING DATE: 2002-11-13  
; PRIOR APPLICATION NUMBER: 09/951,938  
; PRIOR FILING DATE: 2001-09-11  
; PRIOR APPLICATION NUMBER: 60/231,841  
; PRIOR FILING DATE: 2000-09-11  
; NUMBER OF SEQ ID NOS: 109  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 75  
; LENGTH: 1424  
; TYPE: RNA  
; ORGANISM: ARTIFICIAL  
; FEATURE:  
; OTHER INFORMATION: Synthesized Sequence  
US-10-447-839A-75

Query Match 100.0%; Score 60; DB 17; Length 1424;  
Best Local Similarity 100.0%; Pred. No. 1.8e-22;  
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGCTCCACCGCCCCCAGCCACGGTGTACCTCGGCCCGCGGACACACAGCGCGGCCCG 60  
Db 1041 GGCTCCACCGCCCCCAGCCACGGTGTACCTCGGCCCGCGGACACACAGCGCGGCCCG 982

## RESULT 3

US-10-778-859-75/c  
; Sequence 75, Application US/10778859  
; Publication No. US20050042209A1  
; GENERAL INFORMATION:  
; APPLICANT: Kufe, Donald W.  
; APPLICANT: Ohno, Tsuneya  
; TITLE OF INVENTION: MUC1 EXTRACELLULAR DOMAIN AND CANCER TREATMENT COMPOSITIONS AND METHODS DERIVED THEREFROM  
; FILE REFERENCE: 1000.05.011  
; CURRENT APPLICATION NUMBER: US/10/778,859  
; CURRENT FILING DATE: 2004-02-13  
; PRIOR APPLICATION NUMBER: 10/293,391  
; PRIOR FILING DATE: 2002-11-13  
; PRIOR APPLICATION NUMBER: 10/447,839  
; PRIOR FILING DATE: 2003-05-29  
; PRIOR APPLICATION NUMBER: 09/951,938  
; PRIOR FILING DATE: 2001-09-11  
; PRIOR APPLICATION NUMBER: 60/231,841  
; PRIOR FILING DATE: 2000-09-11  
; NUMBER OF SEQ ID NOS: 111  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 75  
; LENGTH: 1424  
; TYPE: RNA  
; ORGANISM: ARTIFICIAL  
; FEATURE:  
; OTHER INFORMATION: Synthesized Sequence

## US-10-778-859-75

Query Match 100.0%; Score 60; DB 21; Length 1424;  
Best Local Similarity 100.0%; Pred. No. 1.8e-22;  
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGCTCCACCGCCCCCAGCCACGGTGTACCTCGGCCCGCGGACACACAGCGCGGCCCG 60  
Db 1041 GGCTCCACCGCCCCCAGCCACGGTGTACCTCGGCCCGCGGACACACAGCGCGGCCCG 982

## RESULT 4

US-10-447-839A-20  
; Sequence 20, Application US/10447839A  
; Publication No. US20040018181A1  
; GENERAL INFORMATION:  
; APPLICANT: Kufe, Donald W.  
; APPLICANT: Kharbanda, Surender  
; APPLICANT: Weitman, Steven D.  
; TITLE OF INVENTION: MUC1 INTERFERENCE RNA COMPOSITIONS AND METHODS DERIVED THEREFROM  
; FILE REFERENCE: 1000.05.009  
; CURRENT APPLICATION NUMBER: US/10/447,839A  
; CURRENT FILING DATE: 2003-05-29  
; PRIOR APPLICATION NUMBER: 10/293,391  
; PRIOR FILING DATE: 2002-11-13  
; PRIOR APPLICATION NUMBER: 09/951,938  
; PRIOR FILING DATE: 2001-09-11  
; PRIOR APPLICATION NUMBER: 60/231,841  
; PRIOR FILING DATE: 2000-09-11  
; NUMBER OF SEQ ID NOS: 109  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 20  
; LENGTH: 1428  
; TYPE: RNA  
; ORGANISM: RNA  
US-10-447-839A-20

Query Match 100.0%; Score 60; DB 17; Length 1428;  
Best Local Similarity 93.3%; Pred. No. 1.8e-22;  
Matches 56; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGCTCCACCGCCCCCAGCCACGGTGTACCTCGGCCCGCGGACACACAGCGCGGCCCG 60  
Db 385 GGUCCACCGCCCCCAGCCACGGUGUACCUCCGCCCGCGGACACACAGCGCGGCCCG 444

## RESULT 5

US-10-778-859-20  
; Sequence 20, Application US/10778859  
; Publication No. US20050042209A1  
; GENERAL INFORMATION:  
; APPLICANT: Kufe, Donald W.  
; APPLICANT: Ohno, Tsuneya  
; TITLE OF INVENTION: MUC1 EXTRACELLULAR DOMAIN AND CANCER TREATMENT COMPOSITIONS AND METHODS DERIVED THEREFROM  
; FILE REFERENCE: 1000.05.011  
; CURRENT APPLICATION NUMBER: US/10/778,859  
; CURRENT FILING DATE: 2004-02-13  
; PRIOR APPLICATION NUMBER: 10/293,391  
; PRIOR FILING DATE: 2002-11-13  
; PRIOR APPLICATION NUMBER: 10/447,839  
; PRIOR FILING DATE: 2003-05-29  
; PRIOR APPLICATION NUMBER: 09/951,938  
; PRIOR FILING DATE: 2001-09-11  
; PRIOR APPLICATION NUMBER: 60/231,841  
; PRIOR FILING DATE: 2000-09-11  
; NUMBER OF SEQ ID NOS: 111  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 20  
; LENGTH: 1428  
; TYPE: RNA  
; ORGANISM: RNA  
US-10-778-859-20

Query Match 100.0%; Score 60; DB 21; Length 1428;  
Best Local Similarity 93.3%; Pred. No. 1.8e-22;  
Matches 56; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCTCCACCGCCCCCAGCCCGGTTGTCACCTCGGCCCGGACACAGCGCGGCCCG 60  
DB 385 GGUCCACCGCCCCCAGCCCGGTTGTCACCTCGGCCCGGACACAGCGCGGCCCG 444

## RESULT 6

US-10-057-136-19  
; Sequence 19, Application US/10057136  
; Publication No. US20030021770A1  
; GENERAL INFORMATION:  
; APPLICANT: SCHLOM, JEFFREY  
; APPLICANT: KANTOR, JUDITH  
; APPLICANT: KUFE, DONALD  
; APPLICANT: PANICALI, DENNIS  
; APPLICANT: GRITZ, LINDA  
; TITLE OF INVENTION: RECOMBINANT POX VIRUS FOR IMMUNIZATION AGAINST MUC1  
; FILE REFERENCE: 700953/47113C  
; CURRENT APPLICATION NUMBER: US/10/057,136  
; CURRENT FILING DATE: 2002-01-25  
; PRIOR APPLICATION NUMBER: 09/366,670  
; PRIOR FILING DATE: 1999-08-03  
; PRIOR APPLICATION NUMBER: PCT/US98/03693  
; PRIOR FILING DATE: 1998-02-24  
; PRIOR APPLICATION NUMBER: 60/038,253  
; PRIOR FILING DATE: 1997-02-24  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 19  
; LENGTH: 1527  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-057-136-19

Query Match 100.0%; Score 60; DB 14; Length 1527;  
Best Local Similarity 100.0%; Pred. No. 1.8e-22;  
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCTCCACCGCCCCCAGCCCGGTTGTCACCTCGGCCCGGACACAGCGCGGCCCG 60  
DB 226 GGCTCCACCGCCCCCAGCCCGGTTGTCACCTCGGCCCGGACACAGCGCGGCCCG 285

## RESULT 7

US-10-447-839A-19  
; Sequence 19, Application US/10447839A  
; Publication No. US20040018181A1  
; GENERAL INFORMATION:  
; APPLICANT: Kufe, Donald W.  
; APPLICANT: Kharbada, Surender  
; APPLICANT: Weitman, Steven D.  
; TITLE OF INVENTION: MUC1 INTERFERENCE RNA COMPOSITIONS AND METHODS DERIVED THEREFROM  
; FILE REFERENCE: 1000.05.009  
; CURRENT APPLICATION NUMBER: US/10/447,839A  
; CURRENT FILING DATE: 2003-05-29  
; PRIOR APPLICATION NUMBER: 10/293,391  
; PRIOR FILING DATE: 2002-11-13  
; PRIOR APPLICATION NUMBER: 09/951,938  
; PRIOR FILING DATE: 2001-09-11  
; PRIOR APPLICATION NUMBER: 60/231,841  
; PRIOR FILING DATE: 2000-09-11  
; NUMBER OF SEQ ID NOS: 109  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 19  
; LENGTH: 1799  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-447-839A-19

Query Match 100.0%; Score 60; DB 17; Length 1799;  
Best Local Similarity 93.3%; Pred. No. 1.7e-22;  
Matches 56; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCTCCACCGCCCCCAGCCCGGTTGTCACCTCGGCCCGGACACAGCGCGGCCCG 60  
DB 453 GGUCCACCGCCCCCAGCCCGGTTGTCACCTCGGCCCGGACACAGCGCGGCCCG 512

## RESULT 8

US-10-778-859-19  
; Sequence 19, Application US/10778859  
; Publication No. US20050042209A1  
; GENERAL INFORMATION:  
; APPLICANT: Kufe, Donald W.  
; APPLICANT: Ohno, Tsuneya  
; TITLE OF INVENTION: MUC1 EXTRACELLULAR DOMAIN AND CANCER TREATMENT COMPOSITIONS AND METHODS DERIVED THEREFROM  
; FILE REFERENCE: 1000.05.011  
; CURRENT APPLICATION NUMBER: US/10/778,859  
; CURRENT FILING DATE: 2004-02-13  
; PRIOR APPLICATION NUMBER: 10/293,391  
; PRIOR FILING DATE: 2002-11-13  
; PRIOR APPLICATION NUMBER: 10/447,839  
; PRIOR FILING DATE: 2003-05-29  
; PRIOR APPLICATION NUMBER: 09/951,938  
; PRIOR FILING DATE: 2001-09-11  
; PRIOR APPLICATION NUMBER: 60/231,841  
; PRIOR FILING DATE: 2000-09-11  
; NUMBER OF SEQ ID NOS: 111  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 19  
; LENGTH: 1799  
; TYPE: RNA  
; ORGANISM: RNA  
US-10-778-859-19

Query Match 100.0%; Score 60; DB 21; Length 1799;  
Best Local Similarity 93.3%; Pred. No. 1.7e-22;  
Matches 56; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCTCCACCGCCCCCAGCCCGGTTGTCACCTCGGCCCGGACACAGCGCGGCCCG 60  
DB 453 GGUCCACCGCCCCCAGCCCGGTTGTCACCTCGGCCCGGACACAGCGCGGCCCG 512

## RESULT 9

US-09-964-824A-573  
; Sequence 573, Application US/09964824A  
; Patent No. US20020102531A1  
; GENERAL INFORMATION:  
; APPLICANT: Horrigan, Stephen  
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signature  
; FILE REFERENCE: 689290-73  
; CURRENT FILING DATE: 2001-09-27  
; PRIOR APPLICATION NUMBER: US/60/236,033  
; PRIOR FILING DATE: 2000-09-28  
; PRIOR APPLICATION NUMBER: US/60/236,032  
; PRIOR FILING DATE: 2000-09-28  
; PRIOR APPLICATION NUMBER: US/60/236,028  
; PRIOR FILING DATE: 2000-09-28  
; NUMBER OF SEQ ID NOS: 583  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 573  
; LENGTH: 1804  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-964-824A-573

Query Match 100.0%; Score 60; DB 9; Length 1804;

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Best Local Similarity 100.0%; Pred. No. 1.7e-22;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCTCCACCGCCCGCCAGCCCGGTTGTCACCTCGCGCCCGGACACACGCGCGCCCG 60
Db 457 GGCTCCACCGCCCGCCAGCCCGGTTGTCACCTCGCGCCCGGACACACGCGCGCCCG 516

RESULT 10
US-10-029-517-17
; Sequence 17, Application US/10029517
; Publication No. US20030148969A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; APPLICANT: Susan J. Myers
; TITLE OF INVENTION: ANTISENSE MODULATION OF MUCIN 1, TRANSMEMBRANE EXPRESSION
; FILE REFERENCE: RTS-0352
; CURRENT APPLICATION NUMBER: US/10/029,517
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 107
; SEQ ID NO 17
; LENGTH: 1804
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (73)...(1500)
US-10-029-517-17

Query Match 100.0%; Score 60; DB 15; Length 1804;
Best Local Similarity 100.0%; Pred. No. 1.7e-22;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCTCCACCGCCCGCCAGCCCGGTTGTCACCTCGCGCCCGGACACACGCGCGCCCG 60
Db 457 GGCTCCACCGCCCGCCAGCCCGGTTGTCACCTCGCGCCCGGACACACGCGCGCCCG 516

RESULT 11
US-10-717-597-30
; Sequence 30, Application US/10717597
; Publication No. US20040110221A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Burczynski, Michael E.
; APPLICANT: Twine, Natalie C.
; APPLICANT: Dorner, Andrew J.
; APPLICANT: Trepicchio, William L.
; APPLICANT: Slonim, Donna K.
; APPLICANT: Stover, Jennifer A.
; TITLE OF INVENTION: METHODS FOR DIAGNOSING RCC AND OTHER SOLID TUMORS
; FILE REFERENCE: AML01080L
; CURRENT APPLICATION NUMBER: US/10/717,597
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US 60/459,782
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: US 60/427,982
; PRIOR FILING DATE: 2002-11-21
; NUMBER OF SEQ ID NOS: 4904
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 30
; LENGTH: 1804
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-717-597-30

Query Match 100.0%; Score 60; DB 19; Length 1804;
Best Local Similarity 100.0%; Pred. No. 1.7e-22;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCTCCACCGCCCGCCAGCCCGGTTGTCACCTCGCGCCCGGACACACGCGCGCCCG 60
Db 457 GGCTCCACCGCCCGCCAGCCCGGTTGTCACCTCGCGCCCGGACACACGCGCGCCCG 516
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RESULT 12
US-10-775-920-84
; Sequence 84, Application US/10775920
; Publication No. US20040175744A1
; GENERAL INFORMATION:
; APPLICANT: Merzen Ltd
; TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCES AND CORRESPONDING ENCODED POLYPEPTIDES
; TITLE OF INVENTION: OF PARTICULAR SECRETED AND MEMBRANE-BOUND PROTEINS OVEREXPRESSED
; FILE REFERENCE: Merzen - 0010B
; CURRENT APPLICATION NUMBER: US/10/775,920
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: US 60/447,900
; PRIOR FILING DATE: 2003-02-13
; NUMBER OF SEQ ID NOS: 385
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 84
; LENGTH: 1804
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-775-920-84

Query Match 100.0%; Score 60; DB 19; Length 1804;
Best Local Similarity 100.0%; Pred. No. 1.7e-22;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 GGCTCCACCGCCCGCCAGCCCGGTTGTCACCTCGCGCCCGGACACACGCGCGCCCG 60
Db 457 GGCTCCACCGCCCGCCAGCCCGGTTGTCACCTCGCGCCCGGACACACGCGCGCCCG 516
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RESULT 13
US-10-843-641A-5876
; Sequence 5876, Application US/10843641A
; Publication No. US20050064454A1
; GENERAL INFORMATION:
; APPLICANT: Avalon Pharmaceuticals, Inc.
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
; FILE REFERENCE: Signature Gene Sets
; CURRENT APPLICATION NUMBER: US/10/843,641A
; CURRENT FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: US/09/873,367
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US/09/954,531
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/09/954,456
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,436
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,832
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/964,824
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/09/967,768
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US/09/968,007
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,347
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,708
; PRIOR FILING DATE: 2001-10-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 8447
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5876
; LENGTH: 1804
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-843-641A-5876
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Query Match 100.0%; Score 60; DB 21; Length 1804;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-22;  
 Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 GGCTCCACCGCCCCCGCCAGCCACGGTGTACCTCGGCCCGGACACACAGGCGGCCCCG 60  
 Db 457 GGCTCCACCGCCCCCGCCAGCCACGGTGTACCTCGGCCCGGACACACAGGCGGCCCCG 516

RESULT 14  
 US-10-101-510-339  
 ; Sequence 339, Application US/10101510  
 ; Publication No. US20030148295A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: WAN, JACKSON  
 ; APPLICANT: WANG, YIXIN  
 ; TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE  
 ; FILE REFERENCE: 15117.0012  
 ; CURRENT APPLICATION NUMBER: US/10/101,510  
 ; CURRENT FILING DATE: 2002-03-20  
 ; PRIOR APPLICATION NUMBER: 60/276,947  
 ; PRIOR FILING DATE: 2001-03-20  
 ; NUMBER OF SEQ ID NOS: 805  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 339  
 ; LENGTH: 1823  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-101-510-339

Query Match 100.0%; Score 60; DB 15; Length 1823;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-22;  
 Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 GGCTCCACCGCCCCCGCCAGCCACGGTGTACCTCGGCCCGGACACACAGGCGGCCCCG 60  
 Db 457 GGCTCCACCGCCCCCGCCAGCCACGGTGTACCTCGGCCCGGACACACAGGCGGCCCCG 516

RESULT 15  
 US-10-406-317-41  
 ; Sequence 41, Application US/10406317  
 ; Publication No. US20040019195A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Schlom, Jeffrey;  
 ; APPLICANT: Hodge, James;  
 ; APPLICANT: Panicali, Dennis  
 ; TITLE OF INVENTION: A recombinant vector expressing multiple constimulatory  
 ; FILE REFERENCE: 38163-0189  
 ; CURRENT APPLICATION NUMBER: US/10/406,317  
 ; CURRENT FILING DATE: 2003-04-04  
 ; PRIOR APPLICATION NUMBER: US/09/856,988  
 ; PRIOR FILING DATE: 2001-05-30  
 ; PRIOR APPLICATION NUMBER: PCT/US99/26866  
 ; PRIOR FILING DATE: 1999-11-12  
 ; PRIOR APPLICATION NUMBER: 60/111,582  
 ; PRIOR FILING DATE: 1998-12-09  
 ; NUMBER OF SEQ ID NOS: 41  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 41  
 ; LENGTH: 2297  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: VECTOR  
 ; OTHER INFORMATION: SEQUENCE  
 US-10-406-317-41

Query Match 100.0%; Score 60; DB 17; Length 2297;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-22;  
 Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCTCCACCGCCCCCGCCAGCCACGGTGTACCTCGGCCCGGACACACAGGCGGCCCCG 60  
 Db 346 GGCTCCACCGCCCCCGCCAGCCACGGTGTACCTCGGCCCGGACACACAGGCGGCCCCG 405

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Title: US-10-057-136-5

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Minimum DB seq length: 0

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# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	30.0	284	1	US-08-150-203A-2
2	18	30.0	284	1	US-08-454-730-2
3	18	30.0	284	3	US-08-949-788-2
4	18	30.0	1289	2	US-08-344-833-1
5	18	30.0	4190	3	US-08-924-345-1
6	17	28.3	1110	4	US-09-252-991A-8962
7	17	28.3	1278	4	US-09-252-991A-9043
8	17	28.3	1968	4	US-09-252-991A-8743
9	17	28.3	80161	3	US-09-036-987A-1
10	17	28.3	80161	3	US-09-370-700-1
11	17	28.3	80161	4	US-09-603-207-1
12	16	26.7	25	4	US-09-396-196G-98221
13	16	26.7	25	4	US-09-396-196G-98222
14	16	26.7	327	4	US-09-902-540-4050
15	16	26.7	1122	4	US-09-252-991A-12729
16	16	26.7	1152	4	US-09-252-991A-12886
17	16	26.7	3772	4	US-09-963-333-5
18	16	26.7	3772	4	US-09-963-333-5
19	16	26.7	3772	4	US-09-962-677-5
20	16	26.7	21511	4	US-09-902-540-1201
21	16	26.7	36241	4	US-08-311-731A-134
22	16	26.7	68750	3	US-09-335-409-1
23	16	26.7	68750	3	US-09-568-102-1
24	16	26.7	68750	3	US-09-567-969-1
25	16	26.7	68750	3	US-09-568-480-1
26	16	26.7	68750	3	US-09-568-486-1
27	16	26.7	68750	3	US-09-568-472-1

c 28	16	26.7	68750	3	US-09-567-999-1	Sequence 1, Appli
c 29	16	26.7	4403785	3	US-09-103-840A-2	Sequence 2, Appli
c 30	16	26.7	4411529	3	US-09-103-840A-1	Sequence 1, Appli
c 31	15	25.0	288	4	US-09-313-294A-741	Sequence 741, App
c 32	15	25.0	292	4	US-09-313-294A-611	Sequence 611, App
c 33	15	25.0	414	4	US-09-252-991A-334	Sequence 334, App
c 34	15	25.0	432	4	US-09-621-976-9152	Sequence 9152, Ap
c 35	15	25.0	437	4	US-09-620-312D-1086	Sequence 1086, Ap
c 36	15	25.0	465	3	US-09-149-476-77	Sequence 77, Appli
c 37	15	25.0	468	4	US-09-252-991A-15459	Sequence 15459, A
c 38	15	25.0	480	4	US-09-252-991A-15417	Sequence 15417, A
c 39	15	25.0	771	4	US-09-252-991A-1476	Sequence 1476, Ap
c 40	15	25.0	825	4	US-09-902-540-3887	Sequence 3887, Ap
c 41	15	25.0	828	4	US-09-252-991A-1701	Sequence 1701, Ap
c 42	15	25.0	1014	4	US-09-252-991A-15280	Sequence 15280, A
c 43	15	25.0	1017	4	US-09-252-991A-15357	Sequence 15357, A
c 44	15	25.0	1071	4	US-09-902-540-5623	Sequence 5623, Ap
c 45	15	25.0	1086	4	US-09-902-540-5366	Sequence 5366, Ap

## ALIGNMENTS

RESULT 1  
US-08-150-203A-2  
; Sequence 2, Application US/08150203A  
; Patent No. 5676951  
; GENERAL INFORMATION:  
; APPLICANT: Rijsewijk, Franciscus Antonius Maria  
; APPLICANT: van Oirschot, Johannes Theodorus  
; APPLICANT: Maes, Roger Kamel  
; TITLE OF INVENTION: Bovine Herpesvirus Type 1  
; TITLE OF INVENTION: Deletion Mutants, Vaccines Based  
; TITLE OF INVENTION: Theorem, Diagnostic Kits For  
; TITLE OF INVENTION: Detection Of Bovine Herpesvirus  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hoffmann & Baron  
; STREET: 350 Jericho Turnpike  
; CITY: Jericho  
; STATE: New York  
; COUNTRY: United States of America  
; ZIP: 11753

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette - 3.5 inch,  
MEDIUM TYPE: 1.44 MB Storage  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: MS DOS  
SOFTWARE: WORD PERFECT 6.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/150,203A  
FILING DATE: December 6, 1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA: No. 5676951e  
ATTORNEY/AGENT INFORMATION:  
NAME: Louise A. Poutch  
REGISTRATION NUMBER: 37,133  
REFERENCE/DOCKET NUMBER: 294-22  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (516) 822-3550  
TELEFAX: (516) 822-3582  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 284 nucleotides  
TYPE: nucleotide  
STRANDEDNESS: single  
TOPOLOGY: Linear  
US-08-150-203A-2

Query Match 30.0%; Score 18; DB 1; Length 284;  
Best Local Similarity 100.0%; Pred. No. 7.1;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 41 CCGACACGCGCCCGCTC 58  
 |||||  
 Db 99 CCGACACGCGCCCGCTC 116

## RESULT 2

US-08-454-730-2  
 ; Sequence 2, Application US/08454730  
 ; Patent No. 5789177  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rijsewijk, Franciscus Antonius Maria  
 ; APPLICANT: van Oirschot, Johannes Theodorus  
 ; APPLICANT: Maes, Roger Kamel  
 ; TITLE OF INVENTION: Bovine Herpesvirus Type 1  
 ; TITLE OF INVENTION: Deletion Mutants, Vaccines Based  
 ; TITLE OF INVENTION: Thereon, Diagnostic Kits For  
 ; TITLE OF INVENTION: Detection Of Bovine Herpesvirus  
 ; TITLE OF INVENTION: Type 1  
 ; NUMBER OF SEQUENCES: 16  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Hoffmann & Baron  
 ; STREET: 350 Jericho Turnpike  
 ; CITY: Jericho  
 ; STATE: New York  
 ; COUNTRY: United States of America  
 ; ZIP: 11753  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette - 3.5 inch,  
 ; MEDIUM TYPE: 1.44 MB Storage  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: MS DOS  
 ; SOFTWARE: WORD PERFECT 6.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/454,730  
 ; FILING DATE: May 31, 1995  
 ; CLASSIFICATION: 536  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/150,203  
 ; FILING DATE: December 6, 1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Ronald J. Baron  
 ; REGISTRATION NUMBER: 29,281  
 ; REFERENCE/DOCKET NUMBER: 294-22 DIV  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (516) 822-3550  
 ; TELEFAX: (516) 822-3582  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 284 nucleotides, 94 amino acids  
 ; TYPE: nucleotide and amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: Linear  
 ; US-08-454-730-2

Query Match 30.0%; Score 18; DB 1; Length 284;  
 Best Local Similarity 100.0%; Pred. No. 7.1;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 41 CCGACACGCGCCCGCTC 58  
 |||||  
 Db 99 CCGACACGCGCCCGCTC 116

## RESULT 3

US-08-949-788-2  
 ; Sequence 2, Application US/08949788  
 ; Patent No. 6403097  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rijsewijk, Franciscus Antonius Maria  
 ; APPLICANT: van Oirschot, Johannes Theodorus  
 ; APPLICANT: Maes, Roger Kamel  
 ; TITLE OF INVENTION: Bovine Herpesvirus Type 1

; TITLE OF INVENTION: Deletion Mutants, Vaccines Based  
 ; TITLE OF INVENTION: Thereon, Diagnostic Kits For  
 ; TITLE OF INVENTION: Detection Of Bovine Herpesvirus  
 ; TITLE OF INVENTION: Type 1  
 ; NUMBER OF SEQUENCES: 16  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Hoffmann & Baron  
 ; STREET: 350 Jericho Turnpike  
 ; CITY: Jericho  
 ; STATE: New York  
 ; COUNTRY: United States of America  
 ; ZIP: 11753  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette - 3.5 inch,  
 ; MEDIUM TYPE: 1.44 MB Storage  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: MS DOS  
 ; SOFTWARE: WORD PERFECT 6.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/949,788  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/150,203  
 ; FILING DATE: 22-MAR-1996  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Louise A. Foutch  
 ; REGISTRATION NUMBER: 37,133  
 ; REFERENCE/DOCKET NUMBER: 294-22  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (516) 822-3550  
 ; TELEFAX: (516) 822-3582  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 284 nucleotides  
 ; TYPE: nucleotide  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: Linear  
 ; US-08-949-788-2

Query Match 30.0%; Score 18; DB 3; Length 284;  
 Best Local Similarity 100.0%; Pred. No. 7.1;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 41 CCGACACGCGCCCGCTC 58  
 |||||  
 Db 99 CCGACACGCGCCCGCTC 116

## RESULT 4

US-08-344-833-1  
 ; Sequence 1, Application US/08344833  
 ; Patent No. 5874280  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Keil, G nther  
 ; TITLE OF INVENTION: Recombinant Bovine Herpesvirus  
 ; TITLE OF INVENTION: vaccine  
 ; NUMBER OF SEQUENCES: 2  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Organon Teknika Corporation  
 ; STREET: 1330-A Piccard Drive  
 ; CITY: Rockville  
 ; STATE: Maryland  
 ; COUNTRY: U.S.A.  
 ; ZIP: 20850  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/344,833



```

; FILING DATE: 09-AUG-1994
; APPLICATION NUMBER: FR 92 07930
; FILING DATE: 26-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Blackstone, William B.
; REGISTRATION NUMBER: 29.772
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 258-5200
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1289 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Bovine herpesvirus
; NAME/KEY: CDS
; LOCATION: 142..1095
; OTHER INFORMATION: /product= "Protein"
; OTHER INFORMATION: /standard_name= "ORF-1"
; FEATURE:
; NAME/KEY: misc_RNA
; LOCATION: 1..3
; OTHER INFORMATION: /function= "stop-codon giv"
; FEATURE:
; NAME/KEY: misc_RNA
; LOCATION: 4..141
; OTHER INFORMATION: /function= "untranslated"
; OTHER INFORMATION: region"
US-08-344-833-1

Query Match 30.0%; Score 18; DB 2; Length 1289;
Best Local Similarity 100.0%; Pred. No. 5.4; 0; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0;

Oy 41 CCGACACGCGCCCGCTC 58
| | | | | | | | | | | | | | | | | |
Db 461 CCGACACGCGCCCGCTC 478

RESULT 5
US-08-924-345-1
; Sequence 1, Application US/08924345
; Patent No. 6224878
; GENERAL INFORMATION:
; APPLICANT: LEUNG-TACK Patricia
; APPLICANT: LEGASTELOIS Isabelle, Christine, Marie-Andree
; APPLICANT: AUDONNET Jean-Christophe, Francis
; APPLICANT: RIVIERE Michel, Emile, Albert
; TITLE OF INVENTION: Mutants and vaccines of the Infectious
; TITLE OF INVENTION: Bovine Rhinotracheitis virus
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LARSON AND TAYLOR
; STREET: 727 SOUTH TWENTY-THIRD STREET
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/924.345
; FILING DATE: 04-SEP-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/199,172

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; FILING DATE: 09-AUG-1994
; APPLICATION NUMBER: FR 92 07930
; FILING DATE: 26-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: SARRO, THOMAS P.
; REGISTRATION NUMBER: 19396
; REFERENCE/DOCKET NUMBER: XI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 920-7200
; TELEFAX: (703) 892-8428
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4190 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Type 1 Bovine Herpesvirus
; STRAIN: ST
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 172..1311
; OTHER INFORMATION: /function= "envelope glycoprotein"
; OTHER INFORMATION: /product= "glycoprotein g1"
; OTHER INFORMATION: /standard_name= "BHV-1 g1"
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1594..3318
; OTHER INFORMATION: /function= "envelope glycoprotein"
; OTHER INFORMATION: /product= "glycoprotein gE"
; OTHER INFORMATION: /standard_name= "BHV-1 gE"
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 3388..3861
; OTHER INFORMATION: /product= "protein US9"
; OTHER INFORMATION: /standard_name= "BHV US9"
US-08-924-345-1

Query Match 30.0%; Score 18; DB 3; Length 4190;
Best Local Similarity 100.0%; Pred. No. 4.4; 0; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0;

Oy 41 CCGACACGCGCCCGCTC 58
| | | | | | | | | | | | | | | | | |
Db 491 CCGACACGCGCCCGCTC 508

RESULT 6
US-09-252-991A-8962
; Sequence 8962, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 8962
; LENGTH: 1110
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-8962

Query Match 28.3%; Score 17; DB 4; Length 1110;

```

```
; Best Local Similarity 100.0%; Pred. No. 17;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 35 CGGCGCCCGACACGCGC 51
Db 189 CGGCGCCCGACACGCGC 205

RESULT 7
US-09-252-991A-9043/c
; Sequence 9043, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 9043
; LENGTH: 1278
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-9043

Query Match 28.3%; Score 17; DB 4; Length 1278;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 35 CGGCGCCCGACACGCGC 51
Db 1154 CGGCGCCCGACACGCGC 1138

RESULT 8
US-09-252-991A-8743
; Sequence 8743, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 8743
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-8743

Query Match 28.3%; Score 17; DB 4; Length 1968;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 35 CGGCGCCCGACACGCGC 51
Db 875 CGGCGCCCGACACGCGC 891

RESULT 9
US-09-036-987A-1/c
; Sequence 1, Application US/09036987A
```

```
; Patent No. 6143526
; GENERAL INFORMATION:
; APPLICANT: Baltz, Richard H.
; APPLICANT: Broughton, Mary C.
; APPLICANT: Crawford, Kathryn P.
; APPLICANT: Madduri, Krishnamurthy
; APPLICANT: Merlo, Donald J.
; APPLICANT: Treadway, Patti J.
; APPLICANT: Turner, Jan R.
; APPLICANT: Waldron, Clive
; TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide
; TITLE OF INVENTION: Production
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dow AgroSciences LLC Patent Department
; STREET: 9330 Zionsville Road
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: USA
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/036,987A
; FILING DATE: 09-MAR-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Stuart, Donald R
; REGISTRATION NUMBER: 28,479
; REFERENCE/DOCKET NUMBER: 50,608
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317)337-4816
; TELEFAX: (317)337-4847
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 80161 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-036-987A-1

Query Match 28.3%; Score 17; DB 3; Length 80161;
Best Local Similarity 100.0%; Pred. No. 7.8;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CGCGCGCGCTGCGCAGC 25
Db 22486 CGCGCGCGCTGCGCAGC 22470

RESULT 10
US-09-370-700-1/c
; Sequence 1, Application US/09370700
; Patent No. 6274350
; GENERAL INFORMATION:
; APPLICANT: Baltz, Richard H
; APPLICANT: Broughton, Mary C
; APPLICANT: Crawford, Kathryn P
; APPLICANT: Madduri, Krishnamurthy
; APPLICANT: Treadway, Patti J
; APPLICANT: Turner, Jan R
; APPLICANT: Waldron, Clive
; TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide
; FILE REFERENCE: 50489 DIV1
; CURRENT APPLICATION NUMBER: US/09/370,700
; CURRENT FILING DATE: 1999-08-09
; EARLIER APPLICATION NUMBER: US 09/36987
; EARLIER FILING DATE: 1998-03-09
; NUMBER OF SEQ ID NOS: 39
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 80161
; TYPE: DNA
; ORGANISM: Saccharopolyspora spinosa
US-09-370-700-1

Query Match      28.3%; Score 17; DB 3; Length 80161;
Best Local Similarity 100.0%; Pred. No. 7.8;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CGCGCGCGCTCGGCACG 25
Db 22486 CGCGCGCGCTCGGCACG 22470

RESULT 11
US-09-603-207-1/c
; Sequence 1, Application US/09603207B
; Patent No. 6521406
; GENERAL INFORMATION:
; APPLICANT: Baltz, Richard H
; APPLICANT: Broughton, Mary C
; APPLICANT: Crawford, Kathryn P
; APPLICANT: Madduri, Krishnamurthy
; APPLICANT: Treadway, Patti J
; APPLICANT: Turner, Jan R
; APPLICANT: Waldron, Clive
; TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide
; FILE REFERENCE: 50489 DIV1
; CURRENT APPLICATION NUMBER: US/09/603,207B
; CURRENT FILING DATE: 2000-06-23
; EARLIER APPLICATION NUMBER: 09/370,700
; EARLIER FILING DATE: 1998-03-09
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 80161
; TYPE: DNA
; ORGANISM: Saccharopolyspora spinosa
US-09-603-207-1

Query Match      28.3%; Score 17; DB 4; Length 80161;
Best Local Similarity 100.0%; Pred. No. 7.8;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CGCGCGCGCTCGGCACG 25
Db 22486 CGCGCGCGCTCGGCACG 22470

RESULT 12
US-09-396-196G-98221
; Sequence 98221, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 98221
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-98221
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Query Match      26.7%; Score 16; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 CCTGCGCACGGAGTGA 31
Db 6 CCTGCGCACGGAGTGA 21

RESULT 13
US-09-396-196G-98222
; Sequence 98222, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 98222
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-98222

Query Match      26.7%; Score 16; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 CCTGCGCACGGAGTGA 31
Db 3 CCTGCGCACGGAGTGA 18
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RESULT 14
US-09-902-540-4050/c
; Sequence 4050, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 4050
; LENGTH: 327
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-4050

Query Match      26.7%; Score 16; DB 4; Length 327;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 ACCGCGCGCGCTGCGC 22
Db 235 ACCGCGCGCGCTGCGC 220
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```

RESULT 15
US-09-252-991A-12729
; Sequence 12729, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 12729
; LENGTH: 1122
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-12729

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Query Match      26.7%; Score 16; DB 4; Length 1122;
Best Local Similarity 100.0%; Pred. NO. 52;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      10  GCGCCGCTGCGCAGC 25
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Db      1081  GCGCCGCTGCGCAGC 1096
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Search completed: June 30, 2005, 04:03:43  
Job time : 121.2 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 29, 2005, 23:23:45 ; Search time 230.7 Seconds  
(without alignments)  
1625.622 Million cell updates/sec

Title: US-10-057-136-5

Perfect score: 60

Sequence: 1 ggatccacggcgccgtgc.....ccgacacgccccgctccc 60

Scoring table: OLIGO NUC  
Gapop 60.0, Gapext 60.0

Searched: 6067389 seqs, 3125258755 residues

Word size : 0

Total number of hits satisfying chosen parameters: 12134778

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications NA:\*

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq.\*
- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq.\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq.\*
- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq.\*
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- 9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq.\*
- 10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq.\*
- 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq.\*
- 12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq.\*
- 13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq.\*
- 14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq.\*
- 15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq.\*
- 16: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq.\*
- 17: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq.\*
- 18: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq.\*
- 19: /cgn2\_6/ptodata/1/pubpna/US10G\_PUBCOMB.seq.\*
- 20: /cgn2\_6/ptodata/1/pubpna/US10H\_PUBCOMB.seq.\*
- 21: /cgn2\_6/ptodata/1/pubpna/US10I\_PUBCOMB.seq.\*
- 22: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq.\*
- 23: /cgn2\_6/ptodata/1/pubpna/US11A\_PUBCOMB.seq.\*
- 24: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq.\*
- 25: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*
- 26: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	60	100.0	60	14	US-10-057-136-5
2	60	100.0	2297	17	US-10-406-317-41
3	21	35.0	1523	18	US-10-425-114-13416
4	21	35.0	1805	19	US-10-437-963-15539
5	18	30.0	237	11	US-09-864-408A-3271
6	18	30.0	552	19	US-10-767-701-20454
7	17	28.3	403	20	US-10-425-115-125389

Sequence 5, Appl  
Sequence 41, Appl  
Sequence 13416, A  
Sequence 15539, A  
Sequence 3271, Ap  
Sequence 20454, A  
Sequence 125389,

Query Match

100.0%; Score 60; DB 14; Length 60;

#### ALIGNMENTS

#### RESULT 1

US-10-057-136-5  
; Sequence 5, Application US/10057136  
; Publication No. US20030021770A1  
; GENERAL INFORMATION:  
; APPLICANT: SCHLOM, JEFFREY  
; APPLICANT: KANTOR, JUDITH  
; APPLICANT: KUFE, DONALD  
; APPLICANT: PANICALI, DENNIS  
; APPLICANT: GRITZ, LINDA  
; TITLE OF INVENTION: RECOMBINANT POX VIRUS FOR IMMUNIZATION AGAINST MUC1  
; TITLE OF INVENTION: TUMOR-ASSOCIATED ANTIGEN  
; FILE REFERENCE: 700953/47113C  
; CURRENT APPLICATION NUMBER: US/10/057,136  
; CURRENT FILING DATE: 2002-01-25  
; PRIOR APPLICATION NUMBER: 09/366,670  
; PRIOR FILING DATE: 1999-08-03  
; PRIOR APPLICATION NUMBER: PCT/US98/03693  
; PRIOR FILING DATE: 1998-02-24  
; PRIOR APPLICATION NUMBER: 60/038,253  
; PRIOR FILING DATE: 1997-02-24  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 5  
LENGTH: 60  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-057-136-5

8 17 28.3 556 20 US-10-425-115-79825 Sequence 79825, A  
c 9 17 28.3 669 20 US-10-739-930-5219 Sequence 5219, Ap  
c 10 17 28.3 807 20 US-10-472-260-159 Sequence 159, App  
c 11 17 28.3 864 17 US-10-282-122A-13300 Sequence 13300, A  
c 12 17 28.3 897 21 US-10-928-992-89 Sequence 89, Appl  
c 13 17 28.3 1017 17 US-10-369-493-40005 Sequence 40005, A  
c 14 17 28.3 1181 19 US-10-437-963-54065 Sequence 54065, A  
c 15 17 28.3 1356 15 US-10-128-714-2220 Sequence 2220, Ap  
c 16 17 28.3 1362 15 US-10-128-714-7220 Sequence 7220, Ap  
c 17 17 28.3 1411 15 US-10-128-714-1220 Sequence 1220, Ap  
c 18 17 28.3 1411 15 US-10-128-714-6220 Sequence 6220, App  
c 19 17 28.3 3411 15 US-10-128-714-5220 Sequence 520, Ap  
c 20 17 28.3 3411 15 US-10-329-148A-1 Sequence 1, Appli  
c 21 17 28.3 80161 17 US-10-809-189-98221 Sequence 98221, A  
c 22 16 26.7 25 21 US-10-809-189-98222 Sequence 98222, A  
c 23 16 26.7 270 20 US-10-425-115-139852 Sequence 139852, A  
c 24 16 26.7 421 20 US-10-425-115-137245 Sequence 137245, A  
c 25 16 26.7 450 19 US-10-767-701-27455 Sequence 27455, A  
c 26 16 26.7 546 19 US-10-437-963-30788 Sequence 30788, A  
c 27 16 26.7 569 13 US-10-027-632-140046 Sequence 140046, A  
c 28 16 26.7 608 19 US-10-767-701-4719 Sequence 4719, Ap  
c 29 16 26.7 668 19 US-10-437-963-81255 Sequence 81255, A  
c 30 16 26.7 828 15 US-10-156-761-5770 Sequence 5770, Ap  
c 31 16 26.7 1098 19 US-10-437-963-14713 Sequence 14713, A  
c 32 16 26.7 1224 19 US-10-437-963-5514 Sequence 5514, Ap  
c 33 16 26.7 1273 18 US-10-425-114-29003 Sequence 29003, A  
c 34 16 26.7 1278 17 US-10-282-122A-25490 Sequence 25490, A  
c 35 16 26.7 1342 19 US-10-767-701-7398 Sequence 7398, Ap  
c 36 16 26.7 1374 15 US-10-156-761-5020 Sequence 5020, Ap  
c 37 16 26.7 1437 20 US-10-425-115-108474 Sequence 108474, A  
c 38 16 26.7 1571 19 US-10-437-963-16579 Sequence 16579, A  
c 39 16 26.7 1596 17 US-10-353-690-69 Sequence 69, Appl  
c 40 16 26.7 1696 21 US-10-956-157-1776 Sequence 1776, Ap  
c 41 16 26.7 1779 17 US-10-354-437-49 Sequence 49, Appl  
c 42 16 26.7 1833 17 US-10-282-122A-27626 Sequence 27626, A  
c 43 16 26.7 1911 17 US-10-282-122A-29194 Sequence 29194, A  
c 44 16 26.7 1911 17 US-10-282-122A-29194 Sequence 29194, A  
c 45 16 26.7 1911 17 US-10-282-122A-29194 Sequence 29194, A

Best Local Similarity 100.0%; Pred. No. 5.1e-24;  
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGATCCACCGCGCGCTGCGCACGGAGTGACGTGCGGCGCCGACACGCGCGCCGCTCCC 60  
Db 1 GGATCCACCGCGCGCTGCGCACGGAGTGACGTGCGGCGCCGACACGCGCGCCGCTCCC 60

## RESULT 2

US-10-406-317-41  
; Sequence 41, Application US/10406317  
; Publication No. US20040019195A1  
; GENERAL INFORMATION:  
; APPLICANT: Schlom, Jeffrey;  
; APPLICANT: Hodge, James;  
; APPLICANT: Panicali, Dennis  
; TITLE OF INVENTION: A recombinant vector expressing multiple constimulatory  
; TITLE OF INVENTION: molecules and uses thereof  
; FILE REFERENCE: 38163-0189  
; CURRENT APPLICATION NUMBER: US/10/406,317  
; CURRENT FILING DATE: 2003-04-04  
; PRIOR APPLICATION NUMBER: US/09/856,988  
; PRIOR FILING DATE: 2001-05-30  
; PRIOR APPLICATION NUMBER: PCT/US99/26866  
; PRIOR FILING DATE: 1999-11-12  
; PRIOR APPLICATION NUMBER: 60/111,582  
; PRIOR FILING DATE: 1998-12-09  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 41  
; LENGTH: 2297  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: VECTOR  
US-10-406-317-41

Query Match 100.0%; Score 60; DB 17; Length 2297;  
Best Local Similarity 100.0%; Pred. No. 2.2e-24;  
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGATCCACCGCGCGCTGCGCACGGAGTGACGTGCGGCGCCGACACGCGCGCCGCTCCC 60  
Db 466 GGATCCACCGCGCGCTGCGCACGGAGTGACGTGCGGCGCCGACACGCGCGCCGCTCCC 525

## RESULT 3

US-10-425-114-13416  
; Sequence 13416, Application US/10425114  
; Publication No. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E  
; APPLICANT: Tabaska, Jack E  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(5313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 13416  
; LENGTH: 1523  
; TYPE: DNA  
; ORGANISM: Oryza sativa nipponbare  
; FEATURE:  
; OTHER INFORMATION: Clone ID: JC-OSROLIB3475049G05\_FLI  
US-10-425-114-13416

Query Match 35.0%; Score 21; DB 18; Length 1523;

Best Local Similarity 100.0%; Pred. No. 0.024;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 GTGACGTGCGCGCCGACACG 48  
Db 1074 GTGACGTGCGCGCCGACACG 1094

## RESULT 4

US-10-437-963-15539  
; Sequence 15539, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 15539  
; LENGTH: 1805  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_21374C.1  
US-10-437-963-15539

Query Match 35.0%; Score 21; DB 19; Length 1805;  
Best Local Similarity 100.0%; Pred. No. 0.024;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 GTGACGTGCGCGCCGACACG 48  
Db 1356 GTGACGTGCGCGCCGACACG 1376

## RESULT 5

US-09-864-408A-3271/c  
; Sequence 3271, Application US/09864408A  
; Publication No. US20040009474A1  
; GENERAL INFORMATION:  
; APPLICANT: Leach, Martin D.  
; APPLICANT: Shinkets, Richard A.  
; TITLE OF INVENTION: No. US20040009474A1e1 Human Polynucleotides and Polypeptides Enco  
; FILE REFERENCE: 21402-012.  
; CURRENT APPLICATION NUMBER: US/09/864,408A  
; CURRENT FILING DATE: 2001-05-24  
; PRIOR APPLICATION NUMBER: 60/206,690  
; PRIOR FILING DATE: 2000-05-24  
; NUMBER OF SEQ ID NOS: 9068  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3271  
; LENGTH: 237  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-864-408A-3271

Query Match 30.0%; Score 18; DB 11; Length 237;  
Best Local Similarity 100.0%; Pred. No. 1.9;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CCGCGCGCGCTGCGCACG 25  
Db 213 CCGCGCGCGCTGCGCACG 196

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RESULT 6
US-10-767-701-20454/c
; Sequence 20454, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(533535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 20454
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(552)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB5121-012-A1-PF1-C3
; US-10-767-701-20454

Query Match      30.0%; Score 18; DB 19; Length 552;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 39 GCCGACACGCGCCCGC 56
Db 301 GCCGACACGCGCCCGC 284

RESULT 7
US-10-425-115-125389/c
; Sequence 125389, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 125389
; LENGTH: 403
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_45827C.1
; US-10-425-115-125389

Query Match      28.3%; Score 17; DB 20; Length 403;
Best Local Similarity 100.0%; Pred. No. 6;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 CGTCGCGCGCCGACACG 48
Db 155 CGTCGCGCGCCGACACG 139

RESULT 8
US-10-425-115-79825
; Sequence 79825, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: MICROBIOLOGICAL RESEARCH AUTHORITY
; APPLICANT: IMPERIAL COLLEGE INNOVATIONS LIMITED
; TITLE OF INVENTION: IMMUNOGENIC COMMENSAL NEISSERIA SEQUENCES
; FILE REFERENCE: GWS/DUC/23480
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; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 79825
; LENGTH: 556
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(556)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_172826C.1
; US-10-425-115-79825

Query Match      28.3%; Score 17; DB 20; Length 556;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 29 TGACGTCGCGCCCGAC 45
Db 261 TGACGTCGCGCCCGAC 277

RESULT 9
US-10-739-930-5219/c
; Sequence 5219, Application US/10739930
; Publication No. US20040216190A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; FILE REFERENCE: 38-21(53377)B
; CURRENT APPLICATION NUMBER: US/10/739,930
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 11088
; SEQ ID NO 5219
; LENGTH: 669
; TYPE: DNA
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(669)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: TRIAB-23APR03-CLUSTER681618_1
; US-10-739-930-5219

Query Match      28.3%; Score 17; DB 20; Length 669;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGATCCACCGCGCGCC 17
Db 628 GGATCCACCGCGCGCC 612

RESULT 10
US-10-472-260-159/c
; Sequence 159, Application US/10472260
; Publication No. US20040265328A1
; GENERAL INFORMATION:
; APPLICANT: MICROBIOLOGICAL RESEARCH AUTHORITY
; APPLICANT: IMPERIAL COLLEGE INNOVATIONS LIMITED
; TITLE OF INVENTION: IMMUNOGENIC COMMENSAL NEISSERIA SEQUENCES
; FILE REFERENCE: GWS/DUC/23480
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; CURRENT APPLICATION NUMBER: US/10/472,260  
; CURRENT FILING DATE: 2003-09-22  
; NUMBER OF SEQ ID NOS: 199  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 159  
; LENGTH: 807  
; TYPE: DNA  
; ORGANISM: Neisseria meningitidis (group B)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(807)  
; OTHER INFORMATION: shikimate-5-dehydrogenase  
US-10-472-260-159

Query Match 28.3%; Score 17; DB 20; Length 807;  
Best Local Similarity 100.0%; Pred. No. 5.1;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CACCGCGCGCGCTGCGC 22  
Db 405 CACCGCGCGCGCTGCGC 389

RESULT 11  
US-10-282-122A-13300/c  
; Sequence 13300, Application US/10282122A  
; Publication No. US20040029129A1

; GENERAL INFORMATION:  
; APPLICANT: Wang, Liangsu  
; APPLICANT: Zamudio, Carlos  
; APPLICANT: Malone, Cheryl  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari  
; APPLICANT: Zyskind, Judith  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John  
; APPLICANT: Carr, Grant  
; APPLICANT: Yamamoto, Robert  
; APPLICANT: Forsyth, R.  
; APPLICANT: Xu, H.

; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
; FILE REFERENCE: ELITRA.034A  
; CURRENT APPLICATION NUMBER: US/10/282,122A

; CURRENT FILING DATE: 2003-02-20  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR FILING DATE: 2000-09-06  
; PRIOR FILING DATE: 2000-09-06  
; PRIOR FILING DATE: 2000-09-09  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR FILING DATE: 2001-02-16  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 78614

; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 13300  
; LENGTH: 864  
; TYPE: DNA  
; ORGANISM: Burkholderia fungorum  
US-10-282-122A-13300

Query Match 28.3%; Score 17; DB 17; Length 864;  
Best Local Similarity 100.0%; Pred. No. 5;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GATCCACGCGCGCGCT 18  
Db 808 GATCCACGCGCGCGCT 792

RESULT 12  
US-10-928-992-89/c  
; Sequence 89, Application US/10928992  
; Publication No. US20050097639A1

; GENERAL INFORMATION:

; APPLICANT: Nguyen, Henry T

; APPLICANT: Kreps, Joel A

; TITLE OF INVENTION: NUCLEIC ACID MOLECULES FROM RICE CONTROLLING ABIOTIC STRESS  
; FILE REFERENCE: 1392/8/2

; CURRENT APPLICATION NUMBER: US/10/928,992

; CURRENT FILING DATE: 2004-08-27

; PRIOR APPLICATION NUMBER: US 60/498,183

; PRIOR FILING DATE: 2003-08-27

; NUMBER OF SEQ ID NOS: 198

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 89

; LENGTH: 897

; TYPE: DNA

; ORGANISM: Oryza sativa

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(897)

US-10-928-992-89

Query Match 28.3%; Score 17; DB 21; Length 897;  
Best Local Similarity 100.0%; Pred. No. 5;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TCCACGCGCGCGCTGC 20  
Db 217 TCCACGCGCGCGCTGC 201

RESULT 13  
US-10-369-493-40005  
; Sequence 40005, Application US/10369493  
; Publication No. US20030233675A1

; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Goldman, Barry S.

; APPLICANT: Chen, Xianfeng

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; FILE REFERENCE: 38-10(52052)B

; CURRENT APPLICATION NUMBER: US/10/369,493

; CURRENT FILING DATE: 2003-02-28

; PRIOR APPLICATION NUMBER: US 60/360,039

; PRIOR FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374

; SEQ ID NO 40005

; LENGTH: 1017

; TYPE: DNA

; ORGANISM: Xanthomonas campestris

US-10-369-493-40005

Query Match 28.3%; Score 17; DB 17; Length 1017;  
Best Local Similarity 100.0%; Pred. No. 4.9;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 ACCGCGCGCGCTGCGCA 23  
|||||



Db 873 ACCGGCGCGCTGGCA 889

## RESULT 14

US-10-437-963-54065/c  
; Sequence 54065, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kowalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 54065  
; LENGTH: 1181  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_56204C.1  
US-10-437-963-54065

Query Match 28.3%; Score 17; DB 19; Length 1181;  
Best Local Similarity 100.0%; Pred. No. 4.7;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TCCACCGCGCGCCTGC 20

Db 317 TCCACCGCGCGCCTGC 301

## RESULT 15

US-10-128-714-2220/c  
; Sequence 2220, Application US/10128714  
; Publication No. US20030119013A1  
; GENERAL INFORMATION:  
; APPLICANT: Jiang, Bo  
; APPLICANT: Hu, Wenqi  
; APPLICANT: Tishkoff, Daniel  
; APPLICANT: Zamudio, Carlos  
; APPLICANT: Eroshkin, Alexey M  
; APPLICANT: Lemieux, Sebastien M  
; TITLE OF INVENTION: Identification of Essential Genes in *Aspergillus fumigatus* and  
; TITLE OF INVENTION: Methods of Use  
; FILE REFERENCE: 10182-018-999  
; CURRENT APPLICATION NUMBER: US/10/128,714  
; CURRENT FILING DATE: 2002-04-23  
; PRIOR APPLICATION NUMBER: US 60/285,697  
; PRIOR FILING DATE: 2001-04-23  
; PRIOR APPLICATION NUMBER: US 60/287,066  
; PRIOR FILING DATE: 2001-04-27  
; PRIOR APPLICATION NUMBER: US 60/295,890  
; PRIOR FILING DATE: 2001-06-05  
; PRIOR APPLICATION NUMBER: US 60/303,899  
; PRIOR FILING DATE: 2001-07-09  
; PRIOR APPLICATION NUMBER: US 60/316,362  
; PRIOR FILING DATE: 2001-08-31  
; NUMBER OF SEQ ID NOS: 8603  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2220  
; LENGTH: 1356  
; TYPE: DNA  
; ORGANISM: *Aspergillus fumigatus*  
US-10-128-714-2220

Query Match 28.3%; Score 17; DB 15; Length 1356;  
Best Local Similarity 100.0%; Pred. No. 4.5;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CCACCGCGCGCCTGCG 21

Db 468 CCACCGCGCGCCTGCG 452

Search completed: June 30, 2005, 04:42:38  
Job time : 398.7 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 30, 2005, 06:50:10 ; Search time 2133 Seconds  
(without alignments)  
356.908 Million cell updates/sec

Title: US-10-057-136-1

Perfect score: 109

Sequence: 1 GSTAPPAGVTSAPDTRPAP 20

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlh  
-O=/cgn2\_1/USPTO\_spool/US100571136/runat\_29062005\_162123\_11398/app\_query.fasta\_1.199  
-DB=EST -QFMT=fasta -SUPFIX=1 -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US100571136 @CGN 1.1 3437 @runat\_29062005\_162123\_11398 -NCPU=3  
-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAEXT=0.5 -FGAPOP=6  
-FGAEXT=7 -YGAPOP=10 -YGAEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:  
1: gb\_est1:  
2: gb\_est2:  
3: gb\_hic:  
4: gb\_est3:  
5: gb\_est4:  
6: gb\_est5:  
7: gb\_est6:  
8: gb\_gss1:  
9: gb\_gss2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	ID	Description
C 1	109	100.0	330 1	AI925867 wo20d04.x
2	109	100.0	604 4	BM791359 K-EST0071
3	109	100.0	877 5	BU542454 AGENCOURT
4	109	100.0	959 6	CA489836 AGENCOURT
5	109	100.0	1113 5	BU148487 AGENCOURT
6	109	100.0	1130 5	BU542996 AGENCOURT
7	109	100.0	1234 5	BQ36898 AGENCOURT
8	109	100.0	1262 5	BQ935496 AGENCOURT
9	109	100.0	1268 5	BQ943554 AGENCOURT

10	109	100.0	1343	5	BQ920055
11	109	100.0	1349	5	BU152566
12	109	100.0	1420	5	BU542790
13	109	100.0	1531	5	BU543309
14	97	89.0	981	4	BG774910
15	97	89.0	1536	5	BQ923149
16	91	83.5	475	6	CB120860
17	91	83.5	669	6	CB122585
18	91	83.5	1334	5	BQ943809
19	90	82.6	472	4	BM759495
20	88	80.7	166	7	T27692
21	83	76.1	619	4	BI260921
22	83	76.1	1678	4	BG775565
23	64	58.7	926	4	BI754598
C 24	62	56.9	451	4	BG724943
C 25	62	56.9	465	4	BG724531
C 26	62	56.9	705	9	AG043162
27	62	56.9	760	7	CO565665
28	62	56.9	969	5	BU221571
C 29	62	56.9	2448	9	CG756594
30	61	56.0	418	7	CN138277
31	61	56.0	510	9	CC719180
C 32	61	56.0	665	9	CC701843
33	61	56.0	756	9	CC701830
C 34	61	56.0	773	9	CG217984
C 35	61	56.0	818	8	BZ713938
C 36	61	56.0	838	8	BZ534307
37	61	56.0	839	9	CG372937
C 38	61	56.0	928	9	CG260788
39	61	56.0	1049	9	CNS07685
40	61	56.0	1339	8	CC191632
C 41	61	56.0	1343	9	AG185838
42	60.5	55.5	1276	4	BG328273
43	60.5	55.5	1712	4	BG111464
44	60	55.0	445	9	CL928152
45	60	55.0	637	9	AG093550

#### ALIGNMENTS

#### RESULT 1

AI925867/c

LOCUS

DEFINITION

wo20d04.x1 NCI\_CGAP Panl Homo sapiens cDNA clone IMAGE:2455879 3', similar to contains element MSRI MSRI repetitive element ;, mRNA sequence.

ACCESSION

AI925867

VERSION

AI925867.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 330)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

AUTHORS

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

JOURNAL

Unpublished (1997)

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Life Technologies catalog #: 11548-013

Clone Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image.html

Insert Length: 578 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 305.

Location/Qualifiers

1..330

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

AI925867 330 bp mRNA linear EST 08-MAR-2000  
wo20d04.x1 NCI\_CGAP Panl Homo sapiens cDNA clone IMAGE:2455879 3', similar to contains element MSRI MSRI repetitive element ;, mRNA sequence.

AI925867.1 GI:5661831

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 330)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Life Technologies catalog #: 11548-013

Clone Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image.html

Insert Length: 578 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 305.

Location/Qualifiers

1..330

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:2455879"  
 /tissue\_type="adenocarcinoma"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI\_CGAP\_Pan1"  
 /note="Organ: pancreas; Vector: pCMV-SPORT6; Site\_1: SalI;  
 Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
 Average insert size 1.72 kb. Life Technologies catalog #:  
 11548-013"

## ORIGIN

Alignment Scores:  
 Pred. No.: 0.000595 Length: 330  
 Score: 109.00 Matches: 20  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 1 Gaps: 0

US-10-057-136-1 (1-20) x A1925867 (1-330)

Qy 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20  
 |||||  
 Db 316 GGCTCCACCGCCCGCCAGCCAGGTGTACCTCGGCGCCGGACACCGCGGCCCG 257  
 |||||

RESULT 2  
 BM791359 604 bp mRNA linear EST 05-MAR-2002  
 LOCUS K-EST0071342 S21SN520 Homo sapiens cDNA clone S21SN520-14-A06 5',  
 mRNA sequence.

ACCESSION BM791359.1 GI:19139591

VERSION BM791359

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS 1 (bases 1 to 604)  
 Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,  
 Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and  
 Kim,Y.S.

TITLE 21C Frontier Korean EST Project 2001

JOURNAL Unpublished (2002)

COMMENT Contact: Kim YS

Genome Research Center

Korea Research Institute of Bioscience & Biotechnology

52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea

Tel: +82-42-860-4470

Fax: +82-42-860-4409

Email: yongsung@mail.kribb.re.kr

Plate: 14 row: A column: 06

High quality sequence stop: 604.

Location/Qualifiers

## FEATURES

source

1..604  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="S21SN520-14-A06"  
 /sex="F"  
 /tissue\_type="Stomach"  
 /cell\_type="floating aggregates"  
 /cell\_line="SNU-520"  
 /lab\_host="Top10P"

/clone\_lib="S21SN520"  
 /note="Organ: Stomach; Vector: pTZ18RP1; Site\_1: EcoRI;  
 Site\_2: NotI; The poly (A)+ RNA was dephosphorylated with  
 bacterial alkaline phosphatase (BAP) and then decapped  
 with tobacco acid pyrophosphatase (TAP). The decapped  
 intact mRNA was ligated with DNA-RNA linker including EcoR  
 I site by treatment of T4 RNA ligase and the first strand  
 cDNA was synthesized from oligo dT-selected mRNA by  
 priming with dT-tailed vector. The dT-tailed vector was  
 adjusted to have about 60nt. The cDNA vector was  
 circularized with E. coli DNA ligase after digestion of

EcoRI which site is also included in vector. An RNA strand  
 converted to a DNA strand by Okayama-Berg method. The  
 obtained cDNA vectors were used for transformation of  
 competent cells E. coli Top10P by electroporation method.  
 The cDNA libraries constructed by this method are  
 full-length enriched cDNA library."

## ORIGIN

Alignment Scores:  
 Pred. No.: 0.00108 Length: 604  
 Score: 109.00 Matches: 20  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 4 Gaps: 0

US-10-057-136-1 (1-20) x BM791359 (1-604)

Qy 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20  
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 Db 28 GGCTCCACCGCCCGCCAGCCAGGTGTACCTCGGCGCCGGACACCGCGGCCCG 87  
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RESULT 3

BU542454

LOCUS

DEFINITION BU542454 877 bp mRNA linear EST 13-SEP-2002  
 5', mRNA sequence.

ACCESSION BU542454

VERSION BU542454.1 GI:22852937

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS 1 (bases 1 to 877)

TITLE NIH-MGC http://mgc.nci.nih.gov/.

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabbs@mail.nih.gov

Tissue Procurement: DCTD/DTP

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: L1CM2769 row: h column: 02

High quality sequence stop: 760.

Location/Qualifiers

## FEATURES

source

1..877  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:6574322"  
 /tissue\_type="carcinoma, cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_40"  
 /note="Organ: prostate; Vector: pOTB7; Site\_1: XhoI;  
 Site\_2: EcoRI; cDNA made by oligo-dT priming.

Directionally cloned into EcoRI/XhoI sites using the  
 following 5' adaptor: GGCAGGAG(G). Library constructed by  
 Ling Hong in the laboratory of Gerald M. Rubin (University  
 of California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies).  
 Note: this is a NIH\_MGC Library."

## ORIGIN

Alignment Scores:  
 Pred. No.: 0.00155 Length: 877  
 Score: 109.00 Matches: 20  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0

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Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0

US-10-057-136-1 (1-20) x BU542454 (1-877)

Oy 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20
DB 35 GGCTCCACGGCCCCCCCCAGCCAGCGTGTACCTCGGCCCGGACACAGCGCGGCCCG 94

RESULT 4
CA489836 959 bp mRNA linear EST 14-NOV-2002
LOCUS AGENCOURT_10810668 MAPcL Homo sapiens cDNA clone IMAGE:6722324 5',
DEFINITION mRNA sequence.
ACCESSION CA489836
VERSION CA489836.1 GI:24952627
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 959)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LAM14284 row: n column: 20
High quality sequence start: 31
High quality sequence stop: 446.
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Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6722324"
/cell_line="ZR-75-1, MCF7, SK-BR-3, MDA-MB-231,
hTERT-HME1, LNCap"
/lab_host="EMDH10B"
/clone_lib="MAPcL"
/note="Vector: pCMV-SPORT6; Site 1: EcoRV; Site 2: Not I;
Subtracted with brain, liver, lung, kidney and muscle.
Directionally cloned. Priming method: oligo-dT. Average
insert size: 1800 bp. Library amplification: 26,000 fold.
Kristi A. Eglund, James J. Vincent, Robert Strausberg,
Bungkook Lee & Ira Pastan: Discovery of new breast,
cancer genes encoding membrane and secreted proteins.
Manuscript submitted."

ORIGIN
Alignment Scores:
Pred. No.: 0.00169 Length: 959
Score: 109.00 Matches: 20
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-057-136-1 (1-20) x CA489836 (1-959)

Oy 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20
DB 349 GGCTCCACGGCCCCCCCCAGCCAGCGTGTACCTCGGCCCGGACACAGCGCGGCCCG 408

RESULT 5
BUI48487

Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0

US-10-057-136-1 (1-20) x BUI48487 (1-1113)

Oy 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20
DB 30 GGCTCCACGGCCCCCCCCAGCCAGCGTGTACCTCTGCCCCGGACACAGCGCGGCCCG 89

RESULT 6
BUI42996 1130 bp mRNA linear EST 13-SEP-2002
LOCUS AGENCOURT_10338707 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:6574979
DEFINITION 5', mRNA sequence.
ACCESSION BUI42996
VERSION BUI42996.1 GI:22853479
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1130)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

```

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JOURNAL
COMMENT
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution by: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1CM2771 row: c column: 11
High quality sequence start: 27
High quality sequence stop: 246.

FEATURES
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1. 1130
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6574979"
/tissue_type="carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_40"
/notes="Organ: prostate; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN
Alignment Scores:
Pred. No.: 0.00199 Length: 1130
Score: 109.00 Matches: 20
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0

US-10-057-136-1 (1-20) x BU542996 (1-1130)

Qy 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20
Db 69 GGCTCCACCGCCGCCCGCCAGCCAGGTGTCACTCTGCGCCCGGACACGACCGCGCCCG 128

RESULT 7
BQ936898 LOCUS
DEFINITION AGENCOURT_8919110 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:6383855
5', mRNA sequence.
ACCESSION BQ936898
VERSION BQ936898.1 GI:22352281
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution by: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1CM2577 row: o column: 24
High quality sequence stop: 245.

FEATURES
source
1. 1234
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6383855"
/tissue_type="carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_40"
/notes="Organ: prostate; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN
Alignment Scores:
Pred. No.: 0.00217 Length: 1234
Score: 109.00 Matches: 20
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0

US-10-057-136-1 (1-20) x BQ936898 (1-1234)

Qy 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20
Db 30 GGCTCCACCGCCGCCCGCCAGCCAGGTGTCACTCTGCGCCCGGACACGACCGCGCCCG 89

RESULT 8
BQ935496 LOCUS
DEFINITION AGENCOURT_8776475 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:6382088
5', mRNA sequence.
ACCESSION BQ935496
VERSION BQ935496.1 GI:22350879
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution by: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1CM2573 row: f column: 09
High quality sequence start: 46
High quality sequence stop: 157.

FEATURES
source
1. 1262
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6382088"
/tissue_type="carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_40"
/notes="Organ: prostate; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
```

following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

## ORIGIN

Alignment Scores:  
Pred. No.: 0.00222 Length: 1262  
Score: 109.00 Matches: 20  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 5 Gaps: 0

US-10-057-136-1 (1-20) x BQ935496 (1-1262)

Qy 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20  
Db 56 GGCTCCACCGCCCCCGACCCAGCGGTGTACCTGTGCCCCGTGACACGAGCGCGGCCCG 115

RESULT 9  
BQ943354 1268 bp mRNA linear EST 21-AUG-2002  
LOCUS AGENCOURT\_8777815 NIH\_MGC\_40 Homo sapiens cDNA clone IMAGE:6384308  
DEFINITION 5', mRNA sequence.

ACCESSION BQ943354  
VERSION BQ943354.1 GI:22359032  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1268)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-remail.nih.gov  
Tissue Procurement: DCTD/DTF

CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov  
Plate: LICM2579 row: b column: 21  
High quality sequence stop: 177.

## FEATURES

Location/Qualifiers

1. .1268  
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/db\_xref="taxon:9606"  
/clone="IMAGE:6384308"  
/tissue\_type="carcinoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_40"  
/note="Organ: prostate; Vector: pOTB7; Site 1: XhoI;  
Site 2: EcoRI; cDNA made by oligo-dT priming.  
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

## ORIGIN

Alignment Scores:  
Pred. No.: 0.00223 Length: 1268  
Score: 109.00 Matches: 20  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0

## DB:

US-10-057-136-1 (1-20) x BQ943354 (1-1268)

Qy 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20  
Db 90 GGCTCCACCGCCCCCGACCCAGCGGTGTACCTGTGCCCCGTGACACGAGCGCGGCCCG 149

## RESULT 10

BQ920055 1343 bp mRNA linear EST 20-AUG-2002  
LOCUS AGENCOURT\_10031674 NIH\_MGC\_40 Homo sapiens cDNA clone IMAGE:6481609  
DEFINITION 5', mRNA sequence.

ACCESSION BQ920055  
VERSION BQ920055.1 GI:22334753  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1343)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-remail.nih.gov  
Tissue Procurement: DCTD/DTF

CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov  
Plate: LICM2663 row: e column: 02  
High quality sequence start: 56  
High quality sequence stop: 237.

## FEATURES

Location/Qualifiers

1. .1343  
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/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6481609"  
/tissue\_type="carcinoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_40"  
/note="Organ: prostate; Vector: pOTB7; Site 1: XhoI;  
Site 2: EcoRI; cDNA made by oligo-dT priming.  
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

## ORIGIN

Alignment Scores:  
Pred. No.: 0.00236 Length: 1343  
Score: 109.00 Matches: 20  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 5 Gaps: 0

US-10-057-136-1 (1-20) x BQ920055 (1-1343)

Qy 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20  
Db 72 GGCTCCACCGCCCCCGACCCAGCGGTGTACCTGTGCCCCGTGACACGAGCGCGGCCCG 131

## RESULT 11

BUI52566 1349 bp mRNA linear EST 03-SEP-2002  
LOCUS AGENCOURT\_8670683 NIH\_MGC\_40 Homo sapiens cDNA clone IMAGE:6380559  
DEFINITION

```

5', mRNA sequence.
ACCESSION BU152566
VERSION BU152566.1 GI:22666098
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1349)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: DCTD/DTF
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LCM2569 row: f column: 16
High quality sequence stop: 291.
FEATURES
source
1. 1349
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/mol_type="mRNA"
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/clone="IMAGE:6380559"
/tissue_type="carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_40"
/notes="Organ: prostate; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN
Alignment Scores:
Pred. No.: 0.00237 Length: 1349
Score: 109.00 Matches: 20
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0

US-10-057-136-1 (1-20) x BU152566 (1-1349)

Qy 1 GlySerThralaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20
|||||
Db 19 GGCTCCACCGCCGCCACCGCCGCTGCACCTCGGCCGACACGACGCGCCGCG 78

RESULT 12
BU542790 1420 bp mRNA linear EST 13-SEP-2002
LOCUS AGENCOURT_10334841 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:6574725
DEFINITION 5', mRNA sequence.
ACCESSION BU542790
VERSION BU542790.1 GI:22853273
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1420)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.

FEATURES
source
1. 1420
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6574725"
/tissue_type="carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_40"
/notes="Organ: prostate; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN
Alignment Scores:
Pred. No.: 0.00249 Length: 1420
Score: 109.00 Matches: 20
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0

US-10-057-136-1 (1-20) x BU542790 (1-1420)

Qy 1 GlySerThralaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20
|||||
Db 19 GGCTCCACCGCCGCCACCGCCGCTGCACCTCGGCCGACACGACGCGCCGCG 78

RESULT 13
BU543309 1531 bp mRNA linear EST 13-SEP-2002
LOCUS AGENCOURT_10327072 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:6575349
DEFINITION 5', mRNA sequence.
ACCESSION BU543309
VERSION BU543309.1 GI:22853792
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1531)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: DCTD/DTF
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LCM2772 row: b column: 21
High quality sequence stop: 166.
FEATURES
source
1. 1531
/organism="Homo sapiens"

```



/mol\_type="mRNA"  
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 /clone\_lib="NIH\_MGC\_40"  
 /note="Organ: prostate; Vector: pOTB7; Site 1: XhoI;  
 Site 2: EcoRI; cDNA made by oligo-dT priming.  
 Directionally cloned into EcoRI/XhoI sites using the  
 following 5' adaptor: GGCACGAG(G). Library constructed by  
 Ling Hong in the laboratory of Gerald M. Rubin (University  
 of California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies).  
 Note: this is a NIH\_MGC Library."

## ORIGIN

Alignment Scores:  
 Pred. No.: 0.00268 Length: 1531  
 Score: 109.00 Matches: 20  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 5 Gaps: 0

US-10-057-136-1 (1-20) x BUS43309 (1-1531)

Oy 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20  
 Db 30 GGCTCCACCGCCCGCCCGCCACCGTGTACCTTCGCCCCGACACACCGCCGCGCCG 89

## RESULT 14

BG774910  
 LOCUS BG774910 981 bp mRNA linear EST 15-MAY-2001  
 DEFINITION 602649832P1 NIH\_MGC\_40 Homo sapiens cDNA clone IMAGE:4761054 5',  
 mRNA sequence.  
 ACCESSION BG774910 GI:14045227  
 VERSION BG774910.1  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 981)  
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: DCTD/DTP  
 cDNA Library Preparation: Ling Hong/Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Cloned through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLCM1612 row: 0 column: 07  
 High quality sequence stop: 874.  
 Location/Qualifiers

FEATURES  
 source

1. 981  
 /organism="Homo sapiens"  
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 /tissue\_type="carcinoma, cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_40"  
 /note="Organ: prostate; Vector: pOTB7; Site 1: XhoI;  
 Site 2: EcoRI; cDNA made by oligo-dT priming.  
 Directionally cloned into EcoRI/XhoI sites using the  
 following 5' adaptor: GGCACGAG(G). Library constructed by  
 Ling Hong in the laboratory of Gerald M. Rubin (University  
 of California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies)."

Note: this is a NIH\_MGC Library."

ORIGIN  
 Alignment Scores:  
 Pred. No.: 0.0524 Length: 981  
 Score: 97.00 Matches: 18  
 Percent Similarity: 94.74% Conservative: 0  
 Best Local Similarity: 94.74% Mismatches: 1  
 Query Match: 88.99% Indels: 0  
 DB: 4 Gaps: 0

US-10-057-136-1 (1-20) x BG774910 (1-981)

Oy 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAla 19  
 Db 21 GGCTCCACCGCCCGCCCGCCACCGTGTACCTTCGCCCCGACACACCGCCGCGCC 77

## RESULT 15

BQ923149  
 LOCUS BQ923149 1536 bp mRNA linear EST 20-AUG-2002  
 DEFINITION AGENCOURT 8929207 NIH\_MGC\_40 Homo sapiens cDNA clone IMAGE:6484568  
 5', mRNA sequence.  
 ACCESSION BQ923149 GI:22338180  
 VERSION BQ923149.1  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 1536)  
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: DCTD/DTP  
 cDNA Library Preparation: Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Cloned through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLCM2670 row: p column: 09  
 High quality sequence stop: 287.  
 Location/Qualifiers

FEATURES  
 source

1. 1536  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:6484568"  
 /tissue\_type="carcinoma, cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_40"  
 /note="Organ: prostate; Vector: pOTB7; Site 1: XhoI;  
 Site 2: EcoRI; cDNA made by oligo-dT priming.  
 Directionally cloned into EcoRI/XhoI sites using the  
 following 5' adaptor: GGCACGAG(G). Library constructed by  
 Ling Hong in the laboratory of Gerald M. Rubin (University  
 of California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies).  
 Note: this is a NIH\_MGC Library."

## ORIGIN

Alignment Scores:  
 Pred. No.: 0.0814 Length: 1536  
 Score: 97.00 Matches: 18  
 Percent Similarity: 94.74% Conservative: 0  
 Best Local Similarity: 94.74% Mismatches: 1  
 Query Match: 88.99% Indels: 0  
 DB: 5 Gaps: 0

US-10-057-136-1 (1-20) x BQ923149 (1-1536)



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 30, 2005, 07:18:05 ; Search time 1601 Seconds  
(without alignments)  
78.353 Million cell updates/sec

Title: US-10-057-136-1

Perfect score: 109

Sequence: 1 GSTAPPAGVTSAPDTRPAP 20

Scoring table:

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Xgapop 10.0 , Xgapext 0.5	
Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 6313374 seqs, 3136092125 residues

Total number of hits satisfying chosen parameters: 12626748

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2\_1/USPTO\_spool/US10057136/runat\_29062005\_162124\_11430/app\_query.fasta\_1.199  
-DB=Published Applications NA -QFMT=fastap -SUFFIX=rnppb -MINMATCH=0.1  
-LOOPCL=0 -LOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62  
-TRANS=human40.cdi -LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=2000000000 -USER=US10057136 @CEN 1.1 480 @runat\_29062005\_162124\_11430  
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-LONGLOG -DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
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Database :

Published Applications NA:\*

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- 2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq.\*
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- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq.\*
- 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*
- 6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq.\*
- 7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq.\*
- 8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq.\*
- 9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq.\*
- 10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq.\*
- 11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq.\*
- 12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*
- 13: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq.\*
- 14: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq.\*
- 15: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq.\*
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- 18: /cgn2\_6/ptodata/2/pubpna/US10F\_PUBCOMB.seq.\*
- 19: /cgn2\_6/ptodata/2/pubpna/US10G\_PUBCOMB.seq.\*
- 20: /cgn2\_6/ptodata/2/pubpna/US10H\_PUBCOMB.seq.\*
- 21: /cgn2\_6/ptodata/2/pubpna/US10I\_PUBCOMB.seq.\*
- 22: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*
- 23: /cgn2\_6/ptodata/2/pubpna/US11A\_PUBCOMB.seq.\*
- 24: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*
- 25: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*
- 26: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	109	100.0	60	14	US-10-057-136-2
2	109	100.0	60	14	US-10-057-136-4
3	109	100.0	60	14	US-10-057-136-5
4	109	100.0	60	14	US-10-057-136-6
5	109	100.0	60	14	US-10-057-136-7
6	109	100.0	60	14	US-10-057-136-8
7	109	100.0	60	14	US-10-057-136-9
8	109	100.0	60	14	US-10-057-136-10
9	109	100.0	60	14	US-10-057-136-11
10	109	100.0	60	14	US-10-057-136-12
11	109	100.0	120	21	US-10-635-211-3
12	109	100.0	162	21	US-10-635-211-8
13	109	100.0	1424	17	US-10-447-839A-75
14	109	100.0	1424	21	US-10-778-859-75
15	109	100.0	1428	17	US-10-447-839A-20
16	109	100.0	1428	21	US-10-778-859-20
17	109	100.0	1527	14	US-10-057-136-19
18	109	100.0	1761	21	US-10-635-211-1
19	109	100.0	1799	17	US-10-447-839A-19
20	109	100.0	1799	21	US-10-778-859-19
21	109	100.0	1804	9	US-09-964-824A-573
22	109	100.0	1804	15	US-10-029-517-17
23	109	100.0	1804	19	US-10-717-597-30
24	109	100.0	1804	19	US-10-775-920-84
25	109	100.0	1804	21	US-10-843-641A-5876
26	109	100.0	1823	15	US-10-101-510-339
27	109	100.0	2297	17	US-10-406-317-41
28	109	100.0	4139	9	US-09-964-824A-105
29	109	100.0	4139	9	US-09-964-824A-578
30	109	100.0	4139	9	US-09-864-864-334
31	109	100.0	4139	9	US-09-880-107-2121
32	109	100.0	4139	11	US-09-968-007A-751
33	109	100.0	4139	14	US-10-171-311-157
34	109	100.0	4139	15	US-10-177-293-310
35	109	100.0	4139	17	US-10-440-464-155
36	109	100.0	4139	19	US-10-734-564-53
37	109	100.0	4139	19	US-10-775-920-85
38	109	100.0	4139	19	US-10-775-920-85
39	109	100.0	4139	21	US-10-843-641A-5408
40	109	100.0	4139	21	US-10-843-641A-5881
41	109	100.0	4139	21	US-10-843-641A-7221
42	109	100.0	8181	11	US-09-951-938-18
43	109	100.0	8181	17	US-10-447-839A-18
44	109	100.0	8181	21	US-10-778-859-18
45	109	100.0	8186	15	US-10-029-517-19

# ALIGNMENTS

## RESULT 1

US-10-057-136-2  
; Sequence 2, Application US/10057136  
; Publication No. US20030021770A1  
; GENERAL INFORMATION:  
; APPLICANT: SCHLOM, JEFFREY  
; APPLICANT: KANTOR, JUDITH  
; APPLICANT: KUPE, DONALD  
; APPLICANT: PANICALI, DENNIS  
; APPLICANT: GRITZ, LINDA  
; TITLE OF INVENTION: RECOMBINANT POX VIRUS FOR IMMUNIZATION AGAINST MUC1  
; FILE REFERENCE: 700953/47113C  
; CURRENT APPLICATION NUMBER: US/10/057,136  
; CURRENT FILING DATE: 2002-01-25  
; PRIOR APPLICATION NUMBER: 09/366,670

; PRIOR FILING DATE: 1999-08-03  
; PRIOR APPLICATION NUMBER: PCT/US98/03693  
; PRIOR FILING DATE: 1998-02-24  
; PRIOR APPLICATION NUMBER: 60/038,253  
; PRIOR FILING DATE: 1997-02-24  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 60  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-057-136-2

Alignment Scores:  
Pred. No.: 3.04e-07 Length: 60  
Score: 109.00 Matches: 20  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 14 Gaps: 0

US-10-057-136-1 (1-20) x US-10-057-136-2 (1-60)

Qy 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20  
Db 1 GGCTCCACCGCCGCCCGCCACCGGTGTCACTCGGCCCGGACACCGAGCGGCCGCG 60

## RESULT 2

US-10-057-136-4

; Sequence 4, Application US/10057136

; Publication No. US20030021770A1

; GENERAL INFORMATION:

; APPLICANT: SCHLOM, JEFFREY

; APPLICANT: KANTOR, JUDITH

; APPLICANT: KUFE, DONALD

; APPLICANT: PANICALI, DENNIS

; APPLICANT: GRITZ, LINDA

; TITLE OF INVENTION: RECOMBINANT POX VIRUS FOR IMMUNIZATION AGAINST MUC1

; TITLE OF INVENTION: TUMOR-ASSOCIATED ANTIGEN

; FILE REFERENCE: 700953/47113C

; CURRENT APPLICATION NUMBER: US/10/057,136

; CURRENT FILING DATE: 2002-01-25

; PRIOR FILING DATE: 1998-02-24

; PRIOR APPLICATION NUMBER: 60/038,253

; PRIOR FILING DATE: 1999-08-03

; PRIOR APPLICATION NUMBER: PCT/US98/03693

; PRIOR FILING DATE: 1998-02-24

; PRIOR APPLICATION NUMBER: 60/038,253

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 4

; LENGTH: 60

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-057-136-4

Alignment Scores:  
Pred. No.: 3.04e-07 Length: 60  
Score: 109.00 Matches: 20  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 14 Gaps: 0

US-10-057-136-1 (1-20) x US-10-057-136-4 (1-60)

Qy 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20  
Db 1 GGCAGTACTGCACCGCCGACATGGCGTAACTACATCAGCACTGTATACAGACCTGCACCT 60

## RESULT 3

US-10-057-136-5

; Sequence 5, Application US/10057136

; Publication No. US20030021770A1  
; GENERAL INFORMATION:  
; APPLICANT: SCHLOM, JEFFREY  
; APPLICANT: KANTOR, JUDITH  
; APPLICANT: KUFE, DONALD  
; APPLICANT: PANICALI, DENNIS  
; APPLICANT: GRITZ, LINDA  
; TITLE OF INVENTION: RECOMBINANT POX VIRUS FOR IMMUNIZATION AGAINST MUC1  
; TITLE OF INVENTION: TUMOR-ASSOCIATED ANTIGEN  
; FILE REFERENCE: 700953/47113C  
; CURRENT APPLICATION NUMBER: US/10/057,136  
; CURRENT FILING DATE: 2002-01-25  
; PRIOR FILING DATE: 1998-02-24  
; PRIOR APPLICATION NUMBER: 60/038,253  
; PRIOR FILING DATE: 1999-08-03  
; PRIOR APPLICATION NUMBER: PCT/US98/03693  
; PRIOR FILING DATE: 1998-02-24  
; PRIOR APPLICATION NUMBER: 60/038,253  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 60  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-057-136-5

Alignment Scores:  
Pred. No.: 3.04e-07 Length: 60  
Score: 109.00 Matches: 20  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 14 Gaps: 0

US-10-057-136-1 (1-20) x US-10-057-136-5 (1-60)

Qy 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20  
Db 1 GGATCCACCGCGCGCTGCGCAGGAGTGACGTGCGGCGCCGACACGCGCGCTCCC 60

## RESULT 4

US-10-057-136-6

; Sequence 6, Application US/10057136

; Publication No. US20030021770A1

; GENERAL INFORMATION:

; APPLICANT: SCHLOM, JEFFREY

; APPLICANT: KANTOR, JUDITH

; APPLICANT: KUFE, DONALD

; APPLICANT: PANICALI, DENNIS

; APPLICANT: GRITZ, LINDA

; TITLE OF INVENTION: RECOMBINANT POX VIRUS FOR IMMUNIZATION AGAINST MUC1

; TITLE OF INVENTION: TUMOR-ASSOCIATED ANTIGEN

; FILE REFERENCE: 700953/47113C

; CURRENT APPLICATION NUMBER: US/10/057,136

; CURRENT FILING DATE: 2002-01-25

; PRIOR FILING DATE: 1998-02-24

; PRIOR APPLICATION NUMBER: 60/038,253

; PRIOR FILING DATE: 1999-08-03

; PRIOR APPLICATION NUMBER: PCT/US98/03693

; PRIOR FILING DATE: 1998-02-24

; PRIOR APPLICATION NUMBER: 60/038,253

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 6

; LENGTH: 60

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-057-136-6

Alignment Scores:

Pred. No.: 3.04e-07 Length: 60

Score: 109.00 Matches: 20

Percent Similarity: 100.00% Conservative: 0

```
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-10-057-136-1 (1-20) x US-10-057-136-6 (1-60)

Qy 1 GlySerThraProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20
Db 1 GGGTCACAGCTCTCCCGCTCATGGGGTTACTTCTGTCAGATCTCGCCAGCTCCA 60

RESULT 5
US-10-057-136-7
; Sequence 7, Application US/10057136
; Publication No. US20030021770A1
; GENERAL INFORMATION:
; APPLICANT: SCHLOM, JEFFREY
; APPLICANT: KANTOR, JUDITH
; APPLICANT: KUFE, DONALD
; APPLICANT: PANICALI, DENNIS
; APPLICANT: GRITZ, LINDA
; TITLE OF INVENTION: RECOMBINANT POX VIRUS FOR IMMUNIZATION AGAINST MUC1
; FILE OF INVENTION: TUMOR-ASSOCIATED ANTIGEN
; CURRENT APPLICATION NUMBER: US/10/057,136
; CURRENT FILING DATE: 2002-01-25
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: PCT/US98/03693
; PRIOR FILING DATE: 1998-02-24
; PRIOR APPLICATION NUMBER: 60/038,253
; PRIOR FILING DATE: 1997-02-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 7
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-057-136-7

Alignment Scores:
Pred. No.: 3,04e-07 Length: 60
Score: 109.00 Matches: 20
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-10-057-136-1 (1-20) x US-10-057-136-7 (1-60)

Qy 1 GlySerThraProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20
Db 1 GGTTCGACGGCCCCCTGCTCACGGTGTAAACATCCGCCCGGATACCAAGACCGGCCCT 60

RESULT 6
US-10-057-136-8
; Sequence 8, Application US/10057136
; Publication No. US20030021770A1
; GENERAL INFORMATION:
; APPLICANT: SCHLOM, JEFFREY
; APPLICANT: KANTOR, JUDITH
; APPLICANT: KUFE, DONALD
; APPLICANT: PANICALI, DENNIS
; APPLICANT: GRITZ, LINDA
; TITLE OF INVENTION: RECOMBINANT POX VIRUS FOR IMMUNIZATION AGAINST MUC1
; FILE OF INVENTION: TUMOR-ASSOCIATED ANTIGEN
; CURRENT APPLICATION NUMBER: US/10/057,136
; CURRENT FILING DATE: 2002-01-25
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: PCT/US98/03693
; PRIOR FILING DATE: 1998-02-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 8
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-057-136-8

Alignment Scores:
Pred. No.: 3,04e-07 Length: 60
Score: 109.00 Matches: 20
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0
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; PRIOR FILING DATE: 1997-02-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 8
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-057-136-8

Alignment Scores:
Pred. No.: 3,04e-07 Length: 60
Score: 109.00 Matches: 20
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-10-057-136-1 (1-20) x US-10-057-136-8 (1-60)

Qy 1 GlySerThraProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20
Db 1 GGCAGCAGCCGCCCGCCGACACACGGGGTCAAGCGCGCCAGACACTCGACCTGCGCCA 60

RESULT 7
US-10-057-136-9
; Sequence 9, Application US/10057136
; Publication No. US20030021770A1
; GENERAL INFORMATION:
; APPLICANT: SCHLOM, JEFFREY
; APPLICANT: KANTOR, JUDITH
; APPLICANT: KUFE, DONALD
; APPLICANT: PANICALI, DENNIS
; APPLICANT: GRITZ, LINDA
; TITLE OF INVENTION: RECOMBINANT POX VIRUS FOR IMMUNIZATION AGAINST MUC1
; FILE OF INVENTION: TUMOR-ASSOCIATED ANTIGEN
; CURRENT APPLICATION NUMBER: US/10/057,136
; CURRENT FILING DATE: 2002-01-25
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: PCT/US98/03693
; PRIOR FILING DATE: 1998-02-24
; PRIOR APPLICATION NUMBER: 60/038,253
; PRIOR FILING DATE: 1997-02-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 9
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-057-136-9

Alignment Scores:
Pred. No.: 3,04e-07 Length: 60
Score: 109.00 Matches: 20
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-10-057-136-1 (1-20) x US-10-057-136-9 (1-60)

Qy 1 GlySerThraProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20
Db 1 GGAAGTACCGCTCCACCTGCACACGGGGTCAAGCGCGCCAGACACTCGACCTGCGCCA 60

RESULT 8
US-10-057-136-10
; Sequence 10, Application US/10057136
; Publication No. US20030021770A1
; GENERAL INFORMATION:
; APPLICANT: SCHLOM, JEFFREY
; APPLICANT: KANTOR, JUDITH
```

; APPLICANT: KUFU, DONALD  
; APPLICANT: PANICALI, DENNIS  
; APPLICANT: GRITZ, LINDA  
; TITLE OF INVENTION: RECOMBINANT POX VIRUS FOR IMMUNIZATION AGAINST MUC1  
; FILE REFERENCE: 700953/47113C  
; CURRENT FILING DATE: 2002-01-25  
; PRIOR FILING DATE: 1999-08-03  
; PRIOR FILING DATE: 1998-02-24  
; PRIOR FILING DATE: 1997-02-24  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 10  
; LENGTH: 60  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-057-136-10  
Alignment Scores:  
Pred. No.: 3.04e-07 Length: 60  
Score: 109.00 Matches: 20  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 14 Gaps: 0  
US-10-057-136-1 (1-20) x US-10-057-136-10 (1-60)  
Qy 1 GlySerThrAlaProProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20  
Db 1 GGGTCGACTGCCCTCCGCGCATGGTGTGACCTCAGCTCTGACACAAAGCCAGCCCCA 60  
RESULT 9  
US-10-057-136-11  
; Sequence 11, Application US/10057136  
; Publication No. US20030021770A1  
; GENERAL INFORMATION:  
; APPLICANT: SCHLOM, JEFFREY  
; APPLICANT: KANTOR, JUDITH  
; APPLICANT: KUFU, DONALD  
; APPLICANT: PANICALI, DENNIS  
; TITLE OF INVENTION: RECOMBINANT POX VIRUS FOR IMMUNIZATION AGAINST MUC1  
; FILE REFERENCE: 700953/47113C  
; CURRENT FILING DATE: 2002-01-25  
; PRIOR FILING DATE: 1999-08-03  
; PRIOR FILING DATE: 1998-02-24  
; PRIOR FILING DATE: 1997-02-24  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 11  
; LENGTH: 60  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-057-136-11  
Alignment Scores:  
Pred. No.: 3.04e-07 Length: 60  
Score: 109.00 Matches: 20  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 14 Gaps: 0

US-10-057-136-1 (1-20) x US-10-057-136-11 (1-60)  
Qy 1 GlySerThrAlaProProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20  
Db 1 GGTTCACGCGCACCTCCAGCACACGGAGTCACGCTCTGACCCGACACCCGTCGAGTCCG 60  
RESULT 10  
US-10-057-136-12  
; Sequence 12, Application US/10057136  
; Publication No. US20030021770A1  
; GENERAL INFORMATION:  
; APPLICANT: SCHLOM, JEFFREY  
; APPLICANT: KANTOR, JUDITH  
; APPLICANT: KUFU, DONALD  
; APPLICANT: PANICALI, DENNIS  
; TITLE OF INVENTION: RECOMBINANT POX VIRUS FOR IMMUNIZATION AGAINST MUC1  
; FILE REFERENCE: 700953/47113C  
; CURRENT FILING DATE: 2002-01-25  
; PRIOR FILING DATE: 1999-08-03  
; PRIOR FILING DATE: 1998-02-24  
; PRIOR FILING DATE: 1997-02-24  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 12  
; LENGTH: 60  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-057-136-12  
Alignment Scores:  
Pred. No.: 3.04e-07 Length: 60  
Score: 109.00 Matches: 20  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 14 Gaps: 0  
US-10-057-136-1 (1-20) x US-10-057-136-12 (1-60)  
Qy 1 GlySerThrAlaProProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20  
Db 1 GGTAGTACAGCGCACCCGCACATGGCGTCACGAGCGCTCCGATACGAGACCGCGCCT 60  
RESULT 11  
US-10-635-211-3  
; Sequence 3, Application US/10635211  
; Publication No. US20050031649A1  
; GENERAL INFORMATION:  
; APPLICANT: Beijing HYDVA Biotechnology Co. Ltd  
; TITLE OF INVENTION: A recombinant fusion protein comprising BCG heat shock protein 65  
; FILE REFERENCE: FP03012US  
; CURRENT FILING DATE: 2003-08-06  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 3  
; LENGTH: 120  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(120)  
US-10-635-211-3  
Alignment Scores:  
Pred. No.: 5.69e-07 Length: 120

```
Score: 109.00 Matches: 20
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0

US-10-057-136-1 (1-20) x US-10-635-211-3 (1-120)

Qy 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20
Db 1 GGTTCTACCGCTCCGCGGCTCACGGTGTACCTCTGCTCCGGACACCGCTCCGCTCCG 60

RESULT 12
US-10-635-211-8/c
; Sequence 8, Application US/10635211
; Publication No. US20050031649A1
; GENERAL INFORMATION:
; APPLICANT: Beijing HYD-VAX Biotechnology Co. Ltd
; TITLE OF INVENTION: A recombinant fusion protein comprising BCG heat shock protein 63
; TITLE OF INVENTION: and the epitope of MUC1
; FILE REFERENCE: FP03012US
; CURRENT APPLICATION NUMBER: US/10/635,211
; CURRENT FILING DATE: 2003-08-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 8
; LENGTH: 162
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-635-211-8

Alignment Scores:
Pred. No.: 7,46e-07 Length: 162
Score: 109.00 Matches: 20
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0

US-10-057-136-1 (1-20) x US-10-635-211-8 (1-162)

Qy 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20
Db 138 GGTTCTACCGCTCCGCGGCTCACGGTGTACCTCTGCTCCGGACACCGCTCCGCTCCG 79

RESULT 13
US-10-447-839A-75/c
; Sequence 75, Application US/10447839A
; Publication No. US20040018181A1
; GENERAL INFORMATION:
; APPLICANT: Kufe, Donald W.
; APPLICANT: Kharbada, Surender
; APPLICANT: Weitman, Steven D.
; TITLE OF INVENTION: MUC1 INTERFERENCE RNA COMPOSITIONS AND METHODS DERIVED THEREFROM
; FILE REFERENCE: 1000.05.009
; CURRENT APPLICATION NUMBER: US/10/447,839A
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: 10/293,391
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 09/951,938
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: 60/231,841
; PRIOR FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 75
; LENGTH: 1424
; TYPE: RNA
; ORGANISM: ARTIFICIAL
; FEATURE:
; OTHER INFORMATION: Synthesized Sequence
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US-10-447-839A-75
Alignment Scores:
Pred. No.: 5,35e-06 Length: 1424
Score: 109.00 Matches: 20
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-10-057-136-1 (1-20) x US-10-447-839A-75 (1-1424)

Qy 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20
Db 1041 GGCTCCACCGCCCCCGCCAGCCCGGTGTACCTCGGCCCCGGACACCGCCGCCCG 982

RESULT 14
US-10-778-859-75/c
; Sequence 75, Application US/10778859
; Publication No. US20050042209A1
; GENERAL INFORMATION:
; APPLICANT: Kufe, Donald W.
; APPLICANT: Ohno, Tsuneya
; TITLE OF INVENTION: MUC1 EXTRACELLULAR DOMAIN AND CANCER TREATMENT COMPOSITIONS AND
; TITLE OF INVENTION: METHODS DERIVED THEREFROM
; FILE REFERENCE: 1000.05.011
; CURRENT APPLICATION NUMBER: US/10/778,859
; CURRENT FILING DATE: 2004-02-13
; PRIOR APPLICATION NUMBER: 10/293,391
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 10/447,839
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: 09/951,938
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: 60/231,841
; PRIOR FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 75
; LENGTH: 1424
; TYPE: RNA
; ORGANISM: ARTIFICIAL
; FEATURE:
; OTHER INFORMATION: Synthesized Sequence
US-10-778-859-75

Alignment Scores:
Pred. No.: 5,35e-06 Length: 1424
Score: 109.00 Matches: 20
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0

US-10-057-136-1 (1-20) x US-10-778-859-75 (1-1424)

Qy 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20
Db 1041 GGCTCCACCGCCCCCGCCAGCCCGGTGTACCTCGGCCCCGGACACCGCCGCCCG 982

RESULT 15
US-10-447-839A-20
; Sequence 20, Application US/10447839A
; Publication No. US20040018181A1
; GENERAL INFORMATION:
; APPLICANT: Kufe, Donald W.
; APPLICANT: Kharbada, Surender
; APPLICANT: Weitman, Steven D.
; TITLE OF INVENTION: MUC1 INTERFERENCE RNA COMPOSITIONS AND METHODS DERIVED THEREFROM
; FILE REFERENCE: 1000.05.009
; CURRENT APPLICATION NUMBER: US/10/447,839A
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: 10/293,391
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; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 09/951,938
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: 60/231,841
; PRIOR FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 1428
; TYPE: RNA
; ORGANISM: RNA
US-10-447-839A-20
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Alignment Scores:
Pred. No.:          5.36e-06          Length:          1428
Score:             109.00             Matches:          20
Percent Similarity: 100.00%             Conservative:    0
Best Local Similarity: 100.00%           Mismatches:     0
Query Match:       100.00%             Indels:         0
DB:                17                 Gaps:           0
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US-10-057-136-1 (1-20) x US-10-447-839A-20 (1-1428)

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Oy      1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20
Db      385 GGUCCACCGCCCCCCCAGCCACGGUGUCACCUCCGGCCCCGGACACCGAGCCGGCCCCG 444
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Search completed: June 30, 2005, 09:12:19  
Job time : 1601 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 30, 2005, 07:12:04 ; Search time 131 Seconds  
(without alignments)  
249.813 Million cell updates/sec

Title: US-10-057-136-1

Perfect score: 109

Sequence: 1 GSTAPPAHGVTISAPDTRPAP 20

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1202784 .seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2\_1/USPTO.spool/US10057136/runat 29062005 162123 11409/app query.fasta\_1.199  
-DB-Issued Patents NA -QWTF=fastap -SUFFIX=rni -MINWATCH=0.1 -LOPCL=0  
-LOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
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-FGAEXT=7 -YGAPOP=10 -YGAEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents NA:  
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2: /cgn2\_6/ptodata/1/ina/5B.COMB.seq:\*  
3: /cgn2\_6/ptodata/1/ina/6A.COMB.seq:\*  
4: /cgn2\_6/ptodata/1/ina/6B.COMB.seq:\*  
5: /cgn2\_6/ptodata/1/ina/PTCUS.COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	109	100.0	1804	4	US-10-029-517-17
2	109	100.0	8186	4	Sequence 17, Appl
3	104	95.4	1721	4	US-10-029-517-19
4	102	93.6	518	4	Sequence 3, Appl
5	101	92.7	572	4	Sequence 101, App
6	98	89.9	60	4	Sequence 18, Appl
7	97	89.0	981	4	US-10-029-517-18
8	97	89.0	3343	4	Sequence 246, App
9	95	87.2	519	4	Sequence 16, Appl
10	95	87.2	534	4	US-10-029-517-16
11	91	83.5	6192	2	Sequence 102, App
12	91	83.5	6192	3	US-09-646-028-42
					Sequence 46, Appl
					Sequence 1, Appl
					Sequence 1, Appl

13	91	83.5	6192	3	US-09-134-916A-1	Sequence 1, Appl
14	91	83.5	6449	2	US-08-479-537A-4	Sequence 4, Appl
15	91	83.5	6449	3	US-09-083-116-4	Sequence 4, Appl
16	91	83.5	6449	3	US-09-134-916A-4	Sequence 4, Appl
17	61	56.0	819	4	US-09-902-540-5683	Sequence 5683, Ap
18	61	56.0	50725	4	US-09-902-540-1271	Sequence 1271, Ap
19	59	54.1	954	3	US-08-680-506-5	Sequence 5, Appl
20	59	54.1	1347	3	US-08-680-506-8	Sequence 8, Appl
21	59	54.1	1587	3	US-08-680-506-6	Sequence 6, Appl
22	59	54.1	2233	3	US-08-680-506-4	Sequence 2, Appl
23	58	53.2	119981	4	US-09-949-016-11844	Sequence 11844, A
24	58	53.2	119982	4	US-09-949-016-13606	Sequence 13606, A
25	58	53.2	119982	4	US-09-949-016-13606	Sequence 13606, A
26	57.5	52.8	14809	4	US-09-902-540-4753	Sequence 4753, Ap
27	57.5	52.8	14809	4	US-09-902-540-1032	Sequence 1032, Ap
28	57.5	52.8	33529	3	US-09-144-085-3	Sequence 3, Appl
29	56	51.4	9653	4	US-09-949-016-12275	Sequence 12275, A
30	56	51.4	9653	4	US-09-949-016-13090	Sequence 13090, A
31	56	51.4	16427	4	US-09-902-540-1160	Sequence 1160, Ap
32	55.5	50.9	3453	4	US-10-101-464A-861	Sequence 861, App
33	55	50.5	714	4	US-09-252-991A-907	Sequence 907, App
34	55	50.5	1362	4	US-09-489-039A-3117	Sequence 3117, Ap
35	55	50.5	1551	4	US-09-252-991A-1128	Sequence 1128, Ap
36	55	50.5	2115	4	US-09-252-991A-952	Sequence 952, App
37	55	50.5	18159	4	US-09-949-016-12401	Sequence 12401, A
38	55	50.5	18160	4	US-09-949-016-13677	Sequence 13677, A
39	54.5	50.0	41768	4	US-09-902-540-1266	Sequence 1266, Ap
40	54.5	50.0	44479	4	US-09-949-016-17176	Sequence 17176, A
41	54	49.5	407	4	US-09-513-999C-2147	Sequence 2147, Ap
42	54	49.5	603	4	US-09-902-540-8033	Sequence 8033, Ap
43	54	49.5	762	4	US-09-252-991A-11986	Sequence 11986, A
44	54	49.5	1123	4	US-09-252-991A-11956	Sequence 11956, A
45	54	49.5	2073	4	US-09-902-540-5730	Sequence 5730, Ap

#### ALIGNMENTS

##### RESULT 1

US-10-029-517-17  
Sequence 17, Application US/10029517

Patent No. 6716627

GENERAL INFORMATION:

APPLICANT: Kenneth W. Dobie

APPLICANT: Susan J. Myers

TITLE OF INVENTION: ANTISENSE MODULATION OF MUCIN 1, TRANSMEMBRANE EXPRESSION

FILE REFERENCE: RTS-0352

CURRENT APPLICATION NUMBER: US/10/029,517

CURRENT FILING DATE: 2001-12-20

NUMBER OF SEQ ID NOS: 107

SEQ ID NO 17

LENGTH: 1804

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (73)...(1500)

US-10-029-517-17

Alignment Scores:

Pred. No.:	2.86e-05	Length:	1804
Score:	109.00	Matches:	20
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-10-057-136-1 (1-20) x US-10-029-517-17 (1-1804)

Oy 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20

Db 457 GGCTCCACCCGCCCCCCCCAGCCACGGTGTACCTCGGCCCGGACACAGCGGCCGCG 516

##### RESULT 2

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US-10-029-517-19
; Sequence 19, Application US/10029517
; Patent No. 6716627
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; APPLICANT: Susan J. Myers
; TITLE OF INVENTION: ANTISENSE MODULATION OF MUCIN 1, TRANSMEMBRANE EXPRESSION
; FILE REFERENCE: RTS-0352
; CURRENT APPLICATION NUMBER: US/10/029,517
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 107
; SEQ ID NO 19
; LENGTH: 8186
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 6899
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 7155
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 7184
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 7957
; OTHER INFORMATION: unknown
; NAME/KEY: intron
; LOCATION: (2997)...(3498)
; OTHER INFORMATION: intron 1
; NAME/KEY: intron:exon junction
; LOCATION: (3498)...(3499)
; OTHER INFORMATION: intron 1:exon 2
; NAME/KEY: exon
; LOCATION: (3508)...(3599)
; OTHER INFORMATION: exon 2d
; NAME/KEY: exon:intron junction
; LOCATION: (3982)...(3983)
; OTHER INFORMATION: exon 2a:intron 2a
; NAME/KEY: intron:exon junction
; LOCATION: (4205)...(4206)
; OTHER INFORMATION: intron 2c:exon 3c
; NAME/KEY: intron:exon junction
; LOCATION: (4259)...(4260)
; OTHER INFORMATION: intron 2d:exon 3d
; NAME/KEY: exon
; LOCATION: (4260)...(4328)
; OTHER INFORMATION: exon 3d
; NAME/KEY: intron:exon junction
; LOCATION: (4632)...(4633)
; OTHER INFORMATION: intron 3:exon 4
; NAME/KEY: exon
; LOCATION: (4914)...(5035)
; OTHER INFORMATION: exon 5
; NAME/KEY: intron
; LOCATION: (5266)...(6293)
; OTHER INFORMATION: intron 6
US-10-029-517-19
Alignment Scores:
Pred. No.: 0.000151
Score: 109.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 4
Length: 8186
Matches: 20
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0
US-10-057-136-1 (1-20) x US-10-029-517-19 (1-8186)
Qy 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20
Db 3825 GGCTCCACCGCCCCCGCCAGCCCGGTGTACCTCGGCCCGGACACCGAGCGCGCCG 3884

US-10-029-517-3
; Sequence 3, Application US/10029517
; Patent No. 6716627
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; APPLICANT: Susan J. Myers
; TITLE OF INVENTION: ANTISENSE MODULATION OF MUCIN 1, TRANSMEMBRANE EXPRESSION
; FILE REFERENCE: RTS-0352
; CURRENT APPLICATION NUMBER: US/10/029,517
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 107
; SEQ ID NO 3
; LENGTH: 1721
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (58)...(1605)
US-10-029-517-3
Alignment Scores:
Pred. No.: 0.000122
Score: 104.00
Percent Similarity: 95.00%
Best Local Similarity: 95.00%
Query Match: 95.41%
DB: 4
Length: 1721
Matches: 19
Conservative: 0
Mismatch: 1
Indels: 0
Gaps: 0
US-10-057-136-1 (1-20) x US-10-029-517-3 (1-1721)
Qy 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20
Db 442 GGCTCCACCGCCCCCGCCAGCCCGGTGTACCTCGGCCCGGACACCGAGCGCGCCG 501

RESULT 4
US-10-029-517-101
; Sequence 101, Application US/10029517
; Patent No. 6716627
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; APPLICANT: Susan J. Myers
; TITLE OF INVENTION: ANTISENSE MODULATION OF MUCIN 1, TRANSMEMBRANE EXPRESSION
; FILE REFERENCE: RTS-0352
; CURRENT APPLICATION NUMBER: US/10/029,517
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 107
; SEQ ID NO 101
; LENGTH: 518
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-10-029-517-101
Alignment Scores:
Pred. No.: 5.95e-05
Score: 102.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 93.58%
DB: 4
Length: 518
Matches: 19
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0
US-10-057-136-1 (1-20) x US-10-029-517-101 (1-518)
Qy 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAla 19
Db 462 GGCTCCACCGCCCCCGCCAGCCCGGTGTACCTCGGCCCGGACACCGAGCGCGCCG 518

RESULT 5
US-10-029-517-18
; Sequence 18, Application US/10029517
; Patent No. 6716627
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; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF MUCIN 1, TRANSMEMBRANE EXPRESSION
; FILE REFERENCE: RTS-0352
; CURRENT APPLICATION NUMBER: US/10/029,517
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 107
; SEQ ID NO 18
; LENGTH: 572
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (67)...(572)
US-10-029-517-18
Alignment Scores:
Pred. No.: 8,97e-05 Length: 572
Score: 101.00 Matches: 19
Percent Similarity: 95.00% Conservative: 0
Best Local Similarity: 95.00% Mismatches: 1
Query Match: 92.66% Indels: 0
DB: 4 Gaps: 0
US-10-057-136-1 (1-20) x US-10-029-517-18 (1-572)
Qy 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20
Db 478 GGCCTCCACCGCCGCCCAAGCCACCGGTGTACCTCGGCCCGGACACAGCGGCCCG 537
RESULT 6
US-09-475-947A-246
; Sequence 246, Application US/09475947A
; Patent No. 6472154
; GENERAL INFORMATION:
; APPLICANT: Garner, Harold R.
; APPLICANT: Wren, Jonathan D.
; APPLICANT: Minna, John D.
; TITLE OF INVENTION: Polymorphic Repeats in Human Genes
; FILE REFERENCE: UTS0667
; CURRENT APPLICATION NUMBER: US/09/475,947A
; CURRENT FILING DATE: 1999-12-31
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 246
; LENGTH: 60
; TYPE: DNA
; ORGANISM: human
US-09-475-947A-246
Alignment Scores:
Pred. No.: 1.85e-05 Length: 60
Score: 98.00 Matches: 18
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 89.91% Indels: 0
DB: 4 Gaps: 0
US-10-057-136-1 (1-20) x US-09-475-947A-246 (1-60)
Qy 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgPro 18
Db 7 GGCCTCCACCGCCGCCCAAGCCACCGGTGTACCTCGGCCCGGACACAGCGGCCG 60
RESULT 7
US-10-029-517-16
; Sequence 16, Application US/10029517
; Patent No. 6716627
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; APPLICANT: Susan J. Myers
; TITLE OF INVENTION: ANTISENSE MODULATION OF MUCIN 1, TRANSMEMBRANE EXPRESSION
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; FILE REFERENCE: RTS-0352
; CURRENT APPLICATION NUMBER: US/10/029,517
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 107
; SEQ ID NO 16
; LENGTH: 981
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: exon:exon junction
; LOCATION: (464)...(465)
; OTHER INFORMATION: exon 3b:exon 4
US-10-029-517-16
Alignment Scores:
Pred. No.: 0.000541 Length: 981
Score: 97.00 Matches: 18
Percent Similarity: 94.74% Conservative: 0
Best Local Similarity: 94.74% Mismatches: 1
Query Match: 88.99% Indels: 0
DB: 4 Gaps: 0
US-10-057-136-1 (1-20) x US-10-029-517-16 (1-981)
Qy 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAla 19
Db 21 GGCCTCCACCGCCGCCCAAGCCACCGGTGTACCTCGGCCCGGACACAGCGGCCG 77
RESULT 8
US-10-029-517-102
; Sequence 102, Application US/10029517
; Patent No. 6716627
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; APPLICANT: Susan J. Myers
; TITLE OF INVENTION: ANTISENSE MODULATION OF MUCIN 1, TRANSMEMBRANE EXPRESSION
; FILE REFERENCE: RTS-0352
; CURRENT APPLICATION NUMBER: US/10/029,517
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 107
; SEQ ID NO 102
; LENGTH: 3343
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-10-029-517-102
Alignment Scores:
Pred. No.: 0.00208 Length: 3343
Score: 97.00 Matches: 18
Percent Similarity: 94.74% Conservative: 0
Best Local Similarity: 94.74% Mismatches: 1
Query Match: 88.99% Indels: 0
DB: 4 Gaps: 0
US-10-057-136-1 (1-20) x US-10-029-517-102 (1-3343)
Qy 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAla 19
Db 1728 GGCCTCCACCGCCGCCCAAGCCACCGGTGTACCTCGGCCCGGACACAGCGGCCG 1784
RESULT 9
US-09-646-028-42
; Sequence 42, Application US/09646028
; Patent No. 6562347
; GENERAL INFORMATION:
; APPLICANT: Kwak, Larry
; APPLICANT: Biragyn, Arya
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
; TITLE OF INVENTION: CHEMOKINE-TUMOR ANTIGEN FUSION PROTEINS AS CANCER VACCINES
; FILE REFERENCE: 14014.0316/P
; CURRENT APPLICATION NUMBER: US/09/646,028
; CURRENT FILING DATE: 2000-09-12
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; PRIOR APPLICATION NUMBER: 60/077,745
; PRIOR FILING DATE: 1998-03-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 42
; LENGTH: 519
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
US-09-646-028-42

Alignment Scores:
Pred. No.:      0.00049      Length:      519
Score:          95.00      Matches:      20
Percent Similarity: 71.43%      Conservative: 0
Best Local Similarity: 71.43%      Mismatches: 0
Query Match:      87.16%      Indels:      8
DB:              4      Gaps:      1

US-10-057-136-1 (1-20) x US-09-646-028-42 (1-519)
Qy      1 GlySerThrAlaProProAlaHis-----GlyValThrSer 12
      |||||
Db      331 GGTTCCTACTGCTCCGCGGCACACGGTGTAACCTTCGCGCCCTCGACGGTGTAACCTCT 390
      |||||

Qy      13 AlaProAspThrArgProAlaPro 20
      |||||
Db      391 GCCCGGACACTCGCCACGACCG 414

RESULT 10
US-09-646-028-46
; Sequence 46, Application US/09646028
; Patent No. 6562347
; GENERAL INFORMATION:
; APPLICANT: Kwak, Larry
; APPLICANT: Biragyn, Arya
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
; FILE REFERENCE: 14014.0316/P
; CURRENT APPLICATION NUMBER: US/09/646.028
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/077,745
; PRIOR FILING DATE: 1998-03-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 46
; LENGTH: 534
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
US-09-646-028-46

Alignment Scores:
Pred. No.:      0.000506      Length:      534
Score:          95.00      Matches:      20
Percent Similarity: 71.43%      Conservative: 0
Best Local Similarity: 71.43%      Mismatches: 0
Query Match:      87.16%      Indels:      8
DB:              4      Gaps:      1

US-10-057-136-1 (1-20) x US-09-646-028-46 (1-534)
Qy      1 GlySerThrAlaProProAlaHis-----GlyValThrSer 12
      |||||
Db      346 GGTTCCTACTGCTCCGCGGCACACGGTGTAACCTTCGCGCCCTCGACGGTGTAACCTCT 405
      |||||

Qy      13 AlaProAspThrArgProAlaPro 20
      |||||
Db      406 GCCCGGACACTCGCCACGACCG 429

RESULT 11
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US-08-479-537A-1
; Sequence 1, Application US/08479537A
; Patent No. 5861381
; GENERAL INFORMATION:
; APPLICANT: CHAMBER, Pierre
; APPLICANT: KIENY, Marie-Paule
; APPLICANT: LATHE, Richard
; APPLICANT: HAREUVENI, Mara
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION FOR THE
; TITLE OF INVENTION: TREATMENT OR PREVENTION OF A MALIGNANT TUMOR
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,537A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 90/13101
; FILING DATE: 23-OCT-1990
; PRIOR APPLICATION NUMBER: WO PCT/FR91/00835
; APPLICATION NUMBER: US 08/403,576
; FILING DATE: 23-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/039,320
; FILING DATE: 04-APR-1993
; PRIOR APPLICATION NUMBER: US 08/403,576
; FILING DATE: 14-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 017753-025
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6192 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 58..120
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 439..5239
; OTHER INFORMATION: /note="The nucleotides spanning
; OTHER INFORMATION: 439-5239 constitute a repeated region wherein the repeat is 61
; OTHER INFORMATION: nucleotides and encodes 20 amino acids, 17 of which are fixed
; OTHER INFORMATION: The number of such repeats varies from 1 to 80."
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 121..6166
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 457
; OTHER INFORMATION: /note="Nucleotide 457 is X1 = NNN
; OTHER INFORMATION: which is the codon for Pro or Ala wherein Pro = CCT, CCC, CCA
; OTHER INFORMATION: or CCG; and Ala = GCT, GCC, GCA, or GCG."
; FEATURE:
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; NAME/KEY: repeat_region
; LOCATION: 487
; OTHER INFORMATION: /note= "Nucleotide 487 is Y = NNN
; OTHER INFORMATION: which is the codon for Thr or Asn wherein Thr = ACT, ACC, ACA
; OTHER INFORMATION: or ACG; and Asn = AAT or AAC."
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 496
; OTHER INFORMATION: /note= "Nucleotide 496 is X2 = NNN
; OTHER INFORMATION: which is the codon for Pro or Ala wherein Pro = CCT, CCC, CCA
; OTHER INFORMATION: or CCG; and Ala = GCT, GCC, GCA, or GCG."
US-08-479-537A-1

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Pred. No.: 0.0249 Length: 6192
Score: 91.00 Matches: 17
Percent Similarity: 85.00% Conservative: 0
Best Local Similarity: 85.00% Mismatches: 3
Query Match: 83.49% Indels: 0
DB: 2 Gaps: 0

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Db 442 GGCCTCCACCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCGNNNAGCCGNNCCG 501

RESULT 12
US-09-083-116-1
; Sequence 1, Application US/09083116
; Patent No. 6203795
; GENERAL INFORMATION:
; APPLICANT: CHAMBERON, Pierre
; APPLICANT: KIENY, Marie-Paule
; APPLICANT: LATHE, Richard
; APPLICANT: HAREUVENI, Mara
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION FOR THE
; TITLE OF INVENTION: TREATMENT OR PREVENTION OF A MALIGNANT TUMOR
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States

COMPUTER TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/083,116
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/479,537
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR91/00835
FILING DATE: 23-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/039,320
FILING DATE: 04-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/403,576
FILING DATE: 14-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 017753-025
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
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; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6192 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 58..120
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 439..5239
; OTHER INFORMATION: /note= "The nucleotides spanning
; OTHER INFORMATION: 439-5239 constitute a repeated region wherein the repeat is 6
; OTHER INFORMATION: nucleotides and encodes 20 amino acids, 17 of which are fixed
; OTHER INFORMATION: The number of such repeats varies from 1 to 80."
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 121..6166
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 457
; OTHER INFORMATION: /note= "Nucleotide 457 is X1 = NNN
; OTHER INFORMATION: which is the codon for Pro or Ala wherein Pro = CCT, CCC, CCA
; OTHER INFORMATION: or CCG; and Ala = GCT, GCC, GCA, or GCG."
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 487
; OTHER INFORMATION: /note= "Nucleotide 487 is Y = NNN
; OTHER INFORMATION: which is the codon for Thr or Asn wherein Thr = ACT, ACC, ACA
; OTHER INFORMATION: or ACG; and Asn = AAT or AAC."
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 496
; OTHER INFORMATION: /note= "Nucleotide 496 is X2 = NNN
; OTHER INFORMATION: which is the codon for Pro or Ala wherein Pro = CCT, CCC, CCA
; OTHER INFORMATION: or CCG; and Ala = GCT, GCC, GCA, or GCG."
US-09-083-116-1

Alignment Scores:
Pred. No.: 0.0249 Length: 6192
Score: 91.00 Matches: 17
Percent Similarity: 85.00% Conservative: 0
Best Local Similarity: 85.00% Mismatches: 3
Query Match: 83.49% Indels: 0
DB: 3 Gaps: 0

US-10-057-136-1 (1-20) x US-09-083-116-1 (1-6192)
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Db 442 GGCCTCCACCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCGNNNAGCCGNNCCG 501

RESULT 13
US-09-134-916A-1
; Sequence 1, Application US/09134916A
; Patent No. 6328956
; GENERAL INFORMATION:
; APPLICANT: CHAMBERON, Pierre
; APPLICANT: KIENY, Marie-Paule
; APPLICANT: LATHE, Richard
; APPLICANT: HAREUVENI, Mara
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION FOR THE
; TITLE OF INVENTION: TREATMENT OR PREVENTION OF A MALIGNANT TUMOR
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
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ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/134,916A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/479,537  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: FR 90/13101  
FILING DATE: 23-OCT-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/FR91/00835  
FILING DATE: 23-OCT-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/039,320  
FILING DATE: 04-APR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/403,576  
FILING DATE: 14-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Teskin, Robin L.  
REGISTRATION NUMBER: 35,030  
REFERENCE/DOCKET NUMBER: 017753-025  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6192 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: sig\_peptide  
LOCATION: 58..120  
FEATURE:  
NAME/KEY: repeat\_region  
LOCATION: 439..5239  
OTHER INFORMATION: /note= "The nucleotides spanning 439-5239 constitute a repeated region wherein the repeat is 6 nucleotides and encodes 20 amino acids, 17 of which are fixed  
OTHER INFORMATION: The number of such repeats varies from 1 to 80."  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 121..6166  
FEATURE:  
NAME/KEY: repeat\_region  
LOCATION: 457  
OTHER INFORMATION: /note= "Nucleotide 457 is X1 = NNN  
OTHER INFORMATION: which is the codon for Pro or Ala wherein Pro = CCT, CCC, CCA  
OTHER INFORMATION: or CCG; and Ala = GCT, GCC, GCA, or GCG."  
FEATURE:  
NAME/KEY: repeat\_region  
LOCATION: 487  
OTHER INFORMATION: /note= "Nucleotide 487 is Y = NNN  
OTHER INFORMATION: which is the codon for Thr or Asn wherein Thr = ACT, ACC, ACA  
OTHER INFORMATION: or ACG; and Asn = AAT or AAC."  
FEATURE:  
NAME/KEY: repeat\_region  
LOCATION: 496  
OTHER INFORMATION: /note= "Nucleotide 496 is X2 = NNN  
OTHER INFORMATION: which is the codon for Pro or Ala wherein Pro = CCT, CCC, CCA  
OTHER INFORMATION: or CCG; and Ala = GCT, GCC, GCA, or GCG."  
US-09-134-916A-1  
Alignment Scores: 0.0249 Length: 6192  
Pred. No.:

Score: 91.00 Matches: 17  
Percent Similarity: 85.00% Conservative: 0  
Best Local Similarity: 85.00% Mismatches: 3  
Query Match: 83.49% Indels: 0  
DB: 3 Gaps: 0  
US-10-057-136-1 (1-20) x US-09-134-916A-1 (1-6192)  
QY 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20  
Db 442 GGCTCCACCGCCCGCCNNNGCCACGGTGTCCCTCGGCCCGGACNNNAGCCGNNCCG 501  
RESULT 14  
US-08-479-537A-4  
Sequence 4, Application US/08479537A  
Patent No. 5861381  
GENERAL INFORMATION:  
APPLICANT: CHAMBER, Pierre  
APPLICANT: KIENY, Marie-Paule  
APPLICANT: LATHE, Richard  
APPLICANT: HAREUVENI, Mara  
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION FOR THE  
TREATMENT OR PREVENTION OF A MALIGNANT TUMOR  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRES:  
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.  
STREET: P.O. Box 1404  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/479,537A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 90/13101  
FILING DATE: 23-OCT-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/FR91/00835  
FILING DATE: 23-OCT-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/039,320  
FILING DATE: 04-APR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/403,576  
FILING DATE: 14-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Teskin, Robin L.  
REGISTRATION NUMBER: 35,030  
REFERENCE/DOCKET NUMBER: 017753-025  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6449 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: sig\_peptide  
LOCATION: 58..120  
FEATURE:  
NAME/KEY: repeat\_region  
LOCATION: 439..5239  
OTHER INFORMATION: /note= "The nucleotides spanning

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; OTHER INFORMATION: 439-5239 constitute a repeated region wherein the repeat is 6
; OTHER INFORMATION: nucleotides and encodes 20 amino acids, 17 of which are fixed
; OTHER INFORMATION: The number of such repeats varies from 1 to 80."
FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 121..5661
;
; NAME/KEY: repeat_region
; LOCATION: 457
;
; OTHER INFORMATION: /note= "Nucleotide 457 is X1 = NNN
; OTHER INFORMATION: which is the codon for Pro or Ala wherein Pro = CCT, CCC, CCA
; OTHER INFORMATION: or CCG; and Ala = GCT, GCC, GCA, or GCG."
FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 487
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; OTHER INFORMATION: /note= "Nucleotide 487 is Y = NNN
; OTHER INFORMATION: which is the codon for Thr or Asn wherein Thr = ACT, ACC, ACA
; OTHER INFORMATION: or ACG; and Asn = AAT or AAC."
FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 496
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; OTHER INFORMATION: /note= "Nucleotide 496 is X2 = NNN
; OTHER INFORMATION: which is the codon for Pro or Ala wherein Pro = CCT, CCC, CCA
; OTHER INFORMATION: or CCG; and Ala = GCT, GCC, GCA, or GCG."
US-08-479-537A-4
Alignment Scores:
Pred. No.: 0.0261 Length: 6449
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Percent Similarity: 85.00% Conservative: 0
Best Local Similarity: 85.00% Mismatches: 3
Query Match: 83.49% Indels: 0
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Db 442 GGCTCCACCGCCCGCCNNNGCCACGGTGTCACCTCGGCCCGCCGACNNNAGCCGNNCCG 501
RESULT 15
US-09-083-116-4
; Sequence 4, Application US/09083116
; Patent No. 6203795
; GENERAL INFORMATION:
; APPLICANT: CHAMBERON, Pierre
; APPLICANT: KIENY, Marie-Paule
; APPLICANT: LATHE, Richard
; APPLICANT: HAREUVENI, Mara
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION FOR THE
; TITLE OF INVENTION: TREATMENT OR PREVENTION OF A MALIGNANT TUMOR
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: US/09/083,116
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/479,537
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR91/00835
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; FILING DATE: 23-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/039,320
; FILING DATE: 04-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/403,576
; FILING DATE: 14-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 017753-025
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6449 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 58..120
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 439..5239
; OTHER INFORMATION: /note= "The nucleotides spanning
; OTHER INFORMATION: 439-5239 constitute a repeated region wherein the repeat is 6
; OTHER INFORMATION: nucleotides and encodes 20 amino acids, 17 of which are fixed
; OTHER INFORMATION: The number of such repeats varies from 1 to 80."
FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 121..5661
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 457
; OTHER INFORMATION: /note= "Nucleotide 457 is X1 = NNN
; OTHER INFORMATION: which is the codon for Pro or Ala wherein Pro = CCT, CCC, CCA
; OTHER INFORMATION: or CCG; and Ala = GCT, GCC, GCA, or GCG."
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; NAME/KEY: repeat_region
; LOCATION: 487
; OTHER INFORMATION: /note= "Nucleotide 487 is Y = NNN
; OTHER INFORMATION: which is the codon for Thr or Asn wherein Thr = ACT, ACC, ACA
; OTHER INFORMATION: or ACG; and Asn = AAT or AAC."
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; NAME/KEY: repeat_region
; LOCATION: 496
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; OTHER INFORMATION: which is the codon for Pro or Ala wherein Pro = CCT, CCC, CCA
; OTHER INFORMATION: or CCG; and Ala = GCT, GCC, GCA, or GCG."
US-09-083-116-4
Alignment Scores:
Pred. No.: 0.0261 Length: 6449
Score: 91.00 Matches: 17
Percent Similarity: 85.00% Conservative: 0
Best Local Similarity: 85.00% Mismatches: 3
Query Match: 83.49% Indels: 0
DB: 3 Gaps: 0
US-10-057-136-1 (1-20) x US-09-083-116-4 (1-6449)
Qy 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20
Db 442 GGCTCCACCGCCCGCCNNNGCCACGGTGTCACCTCGGCCCGCCGACNNNAGCCGNNCCG 501
Search completed: June 30, 2005, 08:45:34
Job time : 134 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 30, 2005, 06:44:14 ; Search time 359 Seconds  
(without alignments)  
329,791 Million cell updates/sec

Title: US-10-057-136-1

Perfect score: 109

Sequence: 1 GSTAPPAHGVTSPDTRPAP 20

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Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 4390206 seqs, 2359870667 residues

Total number of hits satisfying chosen parameters: 8780412

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N\_Geneseq\_16Dec04:\*

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2: Geneseq1990as:*	
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10: Geneseq2007as:*	
11: Geneseq2008as:*	
12: Geneseq2009as:*	
13: Geneseq2010as:*	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	109	100.0	60	2	AAV48321 Nucleotid
3	109	100.0	60	2	AAV48325 Nucleotid
4	109	100.0	60	2	AAV48322 Nucleotid
5	109	100.0	60	2	AAV48324 Nucleotid

RESULT 1  
AAV48320  
ID AAV48320 standard; DNA; 60 BP.  
XX  
AC AAV48320;  
XX  
DT 20-NOV-1998 (first entry)  
XX  
DE Nucleotide sequence encoding MUC1 tandem repeat unit R5.  
XX  
KW ss; MUC1; recombinant pox virus; cytotoxic T-lymphocyte; immunogen;  
XX  
KW tumour; tumour-associated antigen.  
XX  
OS Homo sapiens.  
XX  
FN WO9837095-A2.  
XX  
PD 27-AUG-1998.  
XX  
PF 24-FEB-1998; 98WO-US003693.  
XX  
PR 24-FEB-1997; 97US-0038253P.  
XX  
PA (THER-) THERION BIOLOGICS CORP.  
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
XX (DAND) DANA FARBER CANCER INST INC.  
XX Schlom J, Kantor J, Kufe D, Panicali D, Gritz L;  
PI  
XX

#### ALIGNMENTS

	6	109	100.0	60	2	AAV48318
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	10	109	100.0	60	2	AAV48317
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	13	109	100.0	525	3	AAV48318
	14	109	100.0	891	3	AAV48319
	15	109	100.0	1194	12	ADK68635
	16	109	100.0	1371	3	AAV48317
	17	109	100.0	1378	12	ADK68635
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	21	109	100.0	1457	12	ADK68635
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	23	109	100.0	1614	12	ADK68635
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	25	109	100.0	1634	12	ADK68635
	26	109	100.0	1712	12	ADK68635
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	37	109	100.0	1804	10	ADK68635
	38	109	100.0	1804	12	ADK68635
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	43	109	100.0	1805	13	ADK68635
	44	109	100.0	1808	12	ADK68635
	45	109	100.0	1818	12	ADK68635

DR WPI; 1998-467492/40.  
XX New recombinant pox virus for tumour therapy - comprises DNA encoding an  
PT immunogenic mini-MUC1 fragment comprising 5-25 MUC1 tandem repeat units.  
XX  
XX PS Disclosure; Page 11; 42pp; English.  
XX  
CC The MUC1 tandem repeat units AAV48317-V48325 were used to create an  
CC immunogenic mini-MUC1 fragment for inclusion in a recombinant pox virus  
CC (RPV). The RPV was used in a pharmaceutical composition also containing  
CC an immunomodulator to generate MUC1 specific cytotoxic T-lymphocytes. The  
CC recombinant pox virus therefore encodes an immunogenic MUC1 fragment that  
CC does not undergo significant genetic deletion, thereby providing an  
CC unexpectedly stable and immunogenic pox virus. They can be used to  
CC prevent or treat tumours expressing MUC1 tumour-associated antigens  
XX  
SQ Sequence 60 BP; 9 A; 27 C; 15 G; 9 T; 0 U; 0 Other;  
  
Alignment Scores:  
Pred. No.: 6.26e-06 Length: 60  
Score: 109.00 Matches: 20  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0  
  
US-10-057-136-1 (1-20) x AAV48320 (1-60)  
  
Qy 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20  
Db 1 GGTTCGACGGCCCCCTGCTCACGGTGTACATCCGCCCGGATACCAGACCGGCCCT 60  
  
RESULT 2  
AAV48321  
ID AAV48321 standard; DNA; 60 BP.  
XX  
AC AAV48321;  
XX  
DT 20-NOV-1998 (first entry)  
XX  
DE Nucleotide sequence encoding MUC1 tandem repeat unit R6.  
XX  
KW ss; MUC1; recombinant pox virus; cytotoxic T-lymphocyte; immunogen;  
KW tumour; tumour-associated antigen.  
XX  
OS Homo sapiens.  
XX  
FN WO9837095-A2.  
XX  
PD 27-AUG-1998.  
XX  
PF 24-FEB-1998; 98WO-US003693.  
XX  
PR 24-FEB-1997; 97US-0038253P.  
XX  
XX (THER-) THERION BIOLOGICS CORP.  
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
PA (DAND) DANA FARBER CANCER INST INC.  
XX  
PI Schlom J, Kantor J, Kufe D, Panicali D, Gritz L;  
XX WPI; 1998-467492/40.  
XX  
XX New recombinant pox virus for tumour therapy - comprises DNA encoding an  
PT immunogenic mini-MUC1 fragment comprising 5-25 MUC1 tandem repeat units.  
XX  
XX PS Disclosure; Page 11; 42pp; English.  
XX  
CC The MUC1 tandem repeat units AAV48317-V48325 were used to create an  
CC immunogenic mini-MUC1 fragment for inclusion in a recombinant pox virus  
CC (RPV). The RPV was used in a pharmaceutical composition also containing  
CC an immunomodulator to generate MUC1 specific cytotoxic T-lymphocytes. The  
CC recombinant pox virus therefore encodes an immunogenic MUC1 fragment that

CC does not undergo significant genetic deletion, thereby providing an  
CC unexpectedly stable and immunogenic pox virus. They can be used to  
CC prevent or treat tumours expressing MUC1 tumour-associated antigens  
XX  
SQ Sequence 60 BP; 13 A; 27 C; 17 G; 3 T; 0 U; 0 Other;  
  
Alignment Scores:  
Pred. No.: 6.26e-06 Length: 60  
Score: 109.00 Matches: 20  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0  
  
US-10-057-136-1 (1-20) x AAV48321 (1-60)  
  
Qy 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20  
Db 1 GGCAGCACCGCAGCGCCGCGCACAGCGGGTCAAGCGCGCAGACACTCGACCTGCGCA 60  
  
RESULT 3  
AAV48325  
ID AAV48325 standard; DNA; 60 BP.  
XX  
AC AAV48325;  
XX  
DT 20-NOV-1998 (first entry)  
XX  
DE Nucleotide sequence encoding MUC1 tandem repeat unit R10.  
XX  
KW ss; MUC1; recombinant pox virus; cytotoxic T-lymphocyte; immunogen;  
KW tumour; tumour-associated antigen.  
XX  
OS Homo sapiens.  
XX  
FN WO9837095-A2.  
XX  
PD 27-AUG-1998.  
XX  
PF 24-FEB-1998; 98WO-US003693.  
XX  
PR 24-FEB-1997; 97US-0038253P.  
XX  
XX (THER-) THERION BIOLOGICS CORP.  
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
PA (DAND) DANA FARBER CANCER INST INC.  
XX  
PI Schlom J, Kantor J, Kufe D, Panicali D, Gritz L;  
XX WPI; 1998-467492/40.  
XX  
XX New recombinant pox virus for tumour therapy - comprises DNA encoding an  
PT immunogenic mini-MUC1 fragment comprising 5-25 MUC1 tandem repeat units.  
XX  
XX PS Disclosure; Page 11; 42pp; English.  
XX  
CC The MUC1 tandem repeat units AAV48317-V48325 were used to create an  
CC immunogenic mini-MUC1 fragment for inclusion in a recombinant pox virus  
CC (RPV). The RPV was used in a pharmaceutical composition also containing  
CC an immunomodulator to generate MUC1 specific cytotoxic T-lymphocytes. The  
CC recombinant pox virus therefore encodes an immunogenic MUC1 fragment that  
CC does not undergo significant genetic deletion, thereby providing an  
CC unexpectedly stable and immunogenic pox virus. They can be used to  
CC prevent or treat tumours expressing MUC1 tumour-associated antigens  
XX  
SQ Sequence 60 BP; 12 A; 22 C; 19 G; 7 T; 0 U; 0 Other;  
  
Alignment Scores:  
Pred. No.: 6.26e-06 Length: 60  
Score: 109.00 Matches: 20  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0

```
DB: 2 Gaps: 0
US-10-057-136-1 (1-20) x AAV48325 (1-60)
Oy 1 GlySerThraAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20
Db 1 GGTAGTACAGCGCCACCCGACATGGCGTCACGAGCGTCCGGATACAGACCGCGCCT 60

RESULT 4
AAV48322
ID AAV48322 standard; DNA; 60 BP.
XX
AC AAV48322;
XX
DT 20-NOV-1998 (first entry)
XX
DE Nucleotide sequence encoding MUC1 tandem repeat unit R7.
XX
KW ss; MUC1; recombinant pox virus; cytotoxic T-lymphocyte; immunogen;
XX tumour; tumour-associated antigen.
XX
OS Homo sapiens.
XX
PN WO9837095-A2.
XX
PD 27-AUG-1998.
XX
PF 24-FEB-1998; 98WO-US003693.
XX
PR 24-FEB-1997; 97US-0038253P.
XX
PA (THER-) THERION BIOLOGICS CORP.
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA (DAND ) DANA FARBEN CANCER INST INC.
XX
PI Schlom J, Kantor J, Kufe D, Panicali D, Gritz L;
XX
DR WPI; 1998-467492/40.
XX
PF New recombinant pox virus for tumour therapy - comprises DNA encoding an
PT immunogenic mini-MUC1 fragment comprising 5-25 MUC1 tandem repeat units.
XX
PS Disclosure; Page 11; 42pp; English.
XX
CC The MUC1 tandem repeat units AAV48317-V48325 were used to create an
CC immunogenic mini-MUC1 fragment for inclusion in a recombinant pox virus
CC (RPV). The RPV was used in a pharmaceutical composition also containing
CC an immunomodulator to generate MUC1 specific cytotoxic T-lymphocytes. The
CC recombinant pox virus therefore encodes an immunogenic MUC1 fragment that
CC does not undergo significant genetic deletion, thereby providing an
CC unexpectedly stable and immunogenic pox virus. They can be used to
CC prevent or treat tumours expressing MUC1 tumour-associated antigens
XX
SQ Sequence 60 BP; 14 A; 24 C; 16 G; 6 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6.26e-06 Length: 60
Score: 109.00 Matches: 20
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-057-136-1 (1-20) x AAV48322 (1-60)
Oy 1 GlySerThraAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20
Db 1 GGAAGTACCGCTCCACCTGCACACGGGTCCACAGCGGCCGACACACCTCGCGCCA 60

RESULT 5
AAV48324
ID AAV48324 standard; DNA; 60 BP.
XX
```

```
AC AAV48324;
XX
DT 20-NOV-1998 (first entry)
XX
DE Nucleotide sequence encoding MUC1 tandem repeat unit R9.
XX
KW ss; MUC1; recombinant pox virus; cytotoxic T-lymphocyte; immunogen;
XX tumour; tumour-associated antigen.
XX
OS Homo sapiens.
XX
PN WO9837095-A2.
XX
PD 27-AUG-1998.
XX
PF 24-FEB-1998; 98WO-US003693.
XX
PR 24-FEB-1997; 97US-0038253P.
XX
PA (THER-) THERION BIOLOGICS CORP.
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA (DAND ) DANA FARBEN CANCER INST INC.
XX
PI Schlom J, Kantor J, Kufe D, Panicali D, Gritz L;
XX
DR WPI; 1998-467492/40.
XX
PF New recombinant pox virus for tumour therapy - comprises DNA encoding an
PT immunogenic mini-MUC1 fragment comprising 5-25 MUC1 tandem repeat units.
XX
PS Disclosure; Page 11; 42pp; English.
XX
CC The MUC1 tandem repeat units AAV48317-V48325 were used to create an
CC immunogenic mini-MUC1 fragment for inclusion in a recombinant pox virus
CC (RPV). The RPV was used in a pharmaceutical composition also containing
CC an immunomodulator to generate MUC1 specific cytotoxic T-lymphocytes. The
CC recombinant pox virus therefore encodes an immunogenic MUC1 fragment that
CC does not undergo significant genetic deletion, thereby providing an
CC unexpectedly stable and immunogenic pox virus. They can be used to
CC prevent or treat tumours expressing MUC1 tumour-associated antigens
XX
SQ Sequence 60 BP; 12 A; 26 C; 14 G; 8 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6.26e-06 Length: 60
Score: 109.00 Matches: 20
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-057-136-1 (1-20) x AAV48324 (1-60)
Oy 1 GlySerThraAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20
Db 1 GGTTCAACGGCACCTCCAGCACACGAGTCACTGACCCCGACCCCGTCCAGTCCG 60

RESULT 6
AAV48318
ID AAV48318 standard; DNA; 60 BP.
XX
AC AAV48318;
XX
DT 20-NOV-1998 (first entry)
XX
DE Nucleotide sequence encoding MUC1 tandem repeat unit R3.
XX
KW ss; MUC1; recombinant pox virus; cytotoxic T-lymphocyte; immunogen;
XX tumour; tumour-associated antigen.
XX
OS Homo sapiens.
XX
PN WO9837095-A2.
```

```

XX PD 27-AUG-1998.
XX XX
XX PF 24-FEB-1998; 98WO-US003693.
XX XX
XX PR 24-FEB-1997; 97US-0038253P.
XX XX
XX PA (THER-) THERION BIOLOGICS CORP.
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PA (DAND ) DANA FARBEN CANCER INST INC.
XX PI Schlom J, Kantor J, Kufe D, Panicali D, Gritz L;
XX DR WPI; 1998-467492/40.
XX XX
XX PT New recombinant pox virus for tumour therapy - comprises DNA encoding an
XX PT immunogenic mini-MUC1 fragment comprising 5-25 MUC1 tandem repeat units.
XX PS Disclosure; Page 11; 42pp; English.
XX CC The MUC1 tandem repeat units AAV48317-V48325 were used to create an
XX CC immunogenic mini-MUC1 fragment for inclusion in a recombinant pox virus
XX CC (RPV). The RPV was used in a pharmaceutical composition also containing
XX CC an immunomodulator to generate MUC1 specific cytotoxic T-lymphocytes. The
XX CC recombinant pox virus therefore encodes an immunogenic MUC1 fragment that
XX CC does not undergo significant genetic deletion, thereby providing an
XX CC unexpectedly stable and immunogenic pox virus. They can be used to
XX CC prevent or treat tumours expressing MUC1 tumour-associated antigens
XX XX
XX SQ Sequence 60 BP; 7 A; 29 C; 19 G; 5 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6.26e-06 Length: 60
Score: 109.00 Matches: 20
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-057-136-1 (1-20) x AAV48318 (1-60)

Qy 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20
Db 1 GGATCCACCGCGCGCCCTGCGACGGAGTGCAGTGGCGGCCGACACGCGCCGCTCCC 60

RESULT 7
AAV48323
ID AAV48323 standard; DNA; 60 BP.
AC AAV48323;
XX XX
XX DT 20-NOV-1998 (first entry)
XX DE Nucleotide sequence encoding MUC1 tandem repeat unit R8.
XX KW ss; MUC1; recombinant pox virus; cytotoxic T-lymphocyte; immunogen;
XX KW tumour; tumour-associated antigen.
XX OS Homo sapiens.
XX XX
XX PN WO9837095-A2.
XX XX
XX DE 27-AUG-1998.
XX XX
XX PF 24-FEB-1998; 98WO-US003693.
XX XX
XX PR 24-FEB-1997; 97US-0038253P.
XX XX
XX PA (THER-) THERION BIOLOGICS CORP.
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PA (DAND ) DANA FARBEN CANCER INST INC.
XX PI Schlom J, Kantor J, Kufe D, Panicali D, Gritz L;
XX DR WPI; 1998-467492/40.
XX DR P-PSDB; AAV77229.
XX XX
XX PT New recombinant pox virus for tumour therapy - comprises DNA encoding an
XX PT immunogenic mini-MUC1 fragment comprising 5-25 MUC1 tandem repeat units.
XX PS Disclosure; Page 11; 42pp; English.
XX CC The MUC1 tandem repeat units AAV48317-V48325 were used to create an
XX CC immunogenic mini-MUC1 fragment for inclusion in a recombinant pox virus
XX CC (RPV). The RPV was used in a pharmaceutical composition also containing
XX CC an immunomodulator to generate MUC1 specific cytotoxic T-lymphocytes. The
XX CC recombinant pox virus therefore encodes an immunogenic MUC1 fragment that
XX CC does not undergo significant genetic deletion, thereby providing an
XX CC unexpectedly stable and immunogenic pox virus. They can be used to
XX CC prevent or treat tumours expressing MUC1 tumour-associated antigens
XX XX
XX SQ Sequence 60 BP; 7 A; 29 C; 19 G; 5 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6.26e-06 Length: 60
Score: 109.00 Matches: 20
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-057-136-1 (1-20) x AAV48318 (1-60)

Qy 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20
Db 1 GGATCCACCGCGCGCCCTGCGACGGAGTGCAGTGGCGGCCGACACGCGCCGCTCCC 60

RESULT 7
AAV48323
ID AAV48323 standard; DNA; 60 BP.
AC AAV48323;
XX XX
XX DT 20-NOV-1998 (first entry)
XX DE Nucleotide sequence encoding MUC1 tandem repeat unit R8.
XX KW ss; MUC1; recombinant pox virus; cytotoxic T-lymphocyte; immunogen;
XX KW tumour; tumour-associated antigen.
XX OS Homo sapiens.
XX XX
XX PN WO9837095-A2.
XX XX
XX DE 27-AUG-1998.
XX XX
XX PF 24-FEB-1998; 98WO-US003693.
XX XX
XX PR 24-FEB-1997; 97US-0038253P.
XX XX
XX PA (THER-) THERION BIOLOGICS CORP.
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PA (DAND ) DANA FARBEN CANCER INST INC.
XX PI Schlom J, Kantor J, Kufe D, Panicali D, Gritz L;

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XX WPI; 1998-467492/40.
XX XX
XX PT New recombinant pox virus for tumour therapy - comprises DNA encoding an
XX PT immunogenic mini-MUC1 fragment comprising 5-25 MUC1 tandem repeat units.
XX PS Disclosure; Page 11; 42pp; English.
XX XX
XX CC The MUC1 tandem repeat units AAV48317-V48325 were used to create an
XX CC immunogenic mini-MUC1 fragment for inclusion in a recombinant pox virus
XX CC (RPV). The RPV was used in a pharmaceutical composition also containing
XX CC an immunomodulator to generate MUC1 specific cytotoxic T-lymphocytes. The
XX CC recombinant pox virus therefore encodes an immunogenic MUC1 fragment that
XX CC does not undergo significant genetic deletion, thereby providing an
XX CC unexpectedly stable and immunogenic pox virus. They can be used to
XX CC prevent or treat tumours expressing MUC1 tumour-associated antigens
XX XX
XX SQ Sequence 60 BP; 10 A; 24 C; 17 G; 9 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6.26e-06 Length: 60
Score: 109.00 Matches: 20
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-057-136-1 (1-20) x AAV48323 (1-60)

Qy 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20
Db 1 GGGTCGACTGCCCTCCGGCGCATGGTGTGACCTCAGCTCTGACACAGGCCAGCCCCA 60

RESULT 8
AAV48316
ID AAV48316 standard; cDNA; 60 BP.
AC AAV48316;
XX XX
XX DT 20-NOV-1998 (first entry)
XX DE Nucleotide sequence encoding MUC1 tandem repeat unit.
XX XX
XX KW ss; MUC1; recombinant pox virus; cytotoxic T-lymphocyte; immunogen;
XX KW tumour; tumour-associated antigen.
XX OS Homo sapiens.
XX XX
XX FH Key Location/Qualifiers
XX CDS 1..60
XX FT /*tag= 'a'
XX FT /product= "MUC1 tandem repeat unit"
XX XX
XX PN WO9837095-A2.
XX XX
XX PD 27-AUG-1998.
XX XX
XX PF 24-FEB-1998; 98WO-US003693.
XX XX
XX PR 24-FEB-1997; 97US-0038253P.
XX XX
XX PA (THER-) THERION BIOLOGICS CORP.
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PA (DAND ) DANA FARBEN CANCER INST INC.
XX PI Schlom J, Kantor J, Kufe D, Panicali D, Gritz L;
XX DR WPI; 1998-467492/40.
XX DR P-PSDB; AAV77229.
XX XX
XX PT New recombinant pox virus for tumour therapy - comprises DNA encoding an
XX PT immunogenic mini-MUC1 fragment comprising 5-25 MUC1 tandem repeat units.
XX PS Disclosure; Page 11; 42pp; English.
XX CC The MUC1 tandem repeat units AAV48317-V48325 were used to create an
XX CC immunogenic mini-MUC1 fragment for inclusion in a recombinant pox virus
XX CC (RPV). The RPV was used in a pharmaceutical composition also containing
XX CC an immunomodulator to generate MUC1 specific cytotoxic T-lymphocytes. The
XX CC recombinant pox virus therefore encodes an immunogenic MUC1 fragment that
XX CC does not undergo significant genetic deletion, thereby providing an
XX CC unexpectedly stable and immunogenic pox virus. They can be used to
XX CC prevent or treat tumours expressing MUC1 tumour-associated antigens
XX XX
XX SQ Sequence 60 BP; 10 A; 24 C; 17 G; 9 T; 0 U; 0 Other;

```

PS Example 1; Page 20; 42pp; English.

XX The MUC1 tandem repeat unit was used to create an immunogenic mini-MUC1  
CC fragment for inclusion in a recombinant pox virus (RPV). The RPV was used  
CC in a pharmaceutical composition also containing an immunomodulator to  
CC generate MUC1 specific cytotoxic T-lymphocytes. The recombinant pox virus  
CC therefore encodes an immunogenic MUC1 fragment that does not undergo  
CC significant genetic deletion, thereby providing an unexpectedly stable  
CC and immunogenic pox virus. They can be used to prevent or treat tumours  
CC expressing MUC1 tumour-associated antigens

XX Sequence 60 BP; 7 A; 33 C; 16 G; 4 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 6.26e-06 Length: 60  
Score: 109.00 Matches: 20  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-057-136-1 (1-20) x AAV48316 (1-60)

Oy 1 GlySerThrAlaProProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20  
Db 1 GGCTCCACCGCCCGCCCGACCGGTGTCACTCGCGCCCGACACCGAGCGGCCCG 60

RESULT 9

AAV48319

ID AAV48319 standard; DNA; 60 BP.

XX AAV48319;

XX 20-NOV-1998 (first entry)

XX Nucleotide sequence encoding MUC1 tandem repeat unit R4.

XX ss; MUC1; recombinant pox virus; cytotoxic T-lymphocyte; immunogen;  
KW tumour; tumour-associated antigen.

XX Homo sapiens.

XX WO9837095-A2.

XX 27-AUG-1998.

XX 24-FEB-1998; 98WO-US003693.

XX 24-FEB-1997; 97US-0038253P.

XX (THER-) THERION BIOLOGICS CORP.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
PA (DAND ) DANA FARBER CANCER INST INC.

XX Schlom J, Kantor J, Kufe D, Panicali D, Gritz L;

XX WPI; 1998-467492/40.

XX New recombinant pox virus for tumour therapy - comprises DNA encoding an  
PT immunogenic mini-MUC1 fragment comprising 5-25 MUC1 tandem repeat units.

XX Disclosure; Page 11; 42pp; English.

XX The MUC1 tandem repeat units AAV48317-V48325 were used to create an  
CC immunogenic mini-MUC1 fragment for inclusion in a recombinant pox virus  
CC (RPV). The RPV was used in a pharmaceutical composition also containing  
CC an immunomodulator to generate MUC1 specific cytotoxic T-lymphocytes. The  
CC recombinant pox virus therefore encodes an immunogenic MUC1 fragment that  
CC does not undergo significant genetic deletion, thereby providing an  
CC unexpectedly stable and immunogenic pox virus. They can be used to  
CC prevent or treat tumours expressing MUC1 tumour-associated antigens

XX Sequence 60 BP; 10 A; 23 C; 13 G; 14 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 6.26e-06 Length: 60  
Score: 109.00 Matches: 20  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-057-136-1 (1-20) x AAV48319 (1-60)

Oy 1 GlySerThrAlaProProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20  
Db 1 GGCTCAACAGCTCTCCCGTCACTGGGGTTACTTCTCTCCAGTACTCGCCAGCTCCA 60

RESULT 10

AAV48317

ID AAV48317 standard; DNA; 60 BP.

XX AAV48317;

XX 20-NOV-1998 (first entry)

XX Nucleotide sequence encoding MUC1 tandem repeat unit R2.

XX ss; MUC1; recombinant pox virus; cytotoxic T-lymphocyte; immunogen;  
KW tumour; tumour-associated antigen.

XX Homo sapiens.

XX WO9837095-A2.

XX 27-AUG-1998.

XX 24-FEB-1998; 98WO-US003693.

XX 24-FEB-1997; 97US-0038253P.

XX (THER-) THERION BIOLOGICS CORP.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
PA (DAND ) DANA FARBER CANCER INST INC.

XX Schlom J, Kantor J, Kufe D, Panicali D, Gritz L;

XX WPI; 1998-467492/40.

XX New recombinant pox virus for tumour therapy - comprises DNA encoding an  
PT immunogenic mini-MUC1 fragment comprising 5-25 MUC1 tandem repeat units.

XX Disclosure; Page 11; 42pp; English.

XX The MUC1 tandem repeat units AAV48317-V48325 were used to create an  
CC immunogenic mini-MUC1 fragment for inclusion in a recombinant pox virus  
CC (RPV). The RPV was used in a pharmaceutical composition also containing  
CC an immunomodulator to generate MUC1 specific cytotoxic T-lymphocytes. The  
CC recombinant pox virus therefore encodes an immunogenic MUC1 fragment that  
CC does not undergo significant genetic deletion, thereby providing an  
CC unexpectedly stable and immunogenic pox virus. They can be used to  
CC prevent or treat tumours expressing MUC1 tumour-associated antigens

XX Sequence 60 BP; 17 A; 21 C; 13 G; 9 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 6.26e-06 Length: 60  
Score: 109.00 Matches: 20  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-057-136-1 (1-20) x AAV48317 (1-60)

Oy 1 GlySerThrAlaProProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20

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Db 1 GGCAGTACTGCACCGGCACATGGGTAACATCAGCACCTGATACAGACCTGCACCT 60
|||||
RESULT 11
ADK68635/c
ID ADK68635 standard; cDNA; 156 BP.
XX AC
XX ADK68635;
XX AC
DT 06-MAY-2004 (first entry)
XX
XX HSP65-MUC1 antigen CTL epitope related cDNA #3.
XX
XX Human breast cancer; Mycobacterium bovis; heat shock protein 65; BCG;
XX HSP65; cytotoxic T lymphocyte; CTL; MUC1; HSP65-MUC1 antigen CTL epitope;
XX ss.
XX
XX Unidentified.
XX
XX CN1368384-A.
XX
XX 11-SEP-2002.
XX
XX 08-FEB-2001; 2001CN-00102614.
XX
XX 08-FEB-2001; 2001CN-00102614.
XX
XX (DTWE-) DIWEIHUAYU BIO TECHNOLOGY CO LTD BEIJING.
XX
XX Yu Y, Li H;
XX
XX WPI; 2003-854662/80.
XX
XX Genetically engineered vaccine of MUC-1 antigen for human breast cancer.
XX
XX Example 2; Page 4 (Disclosure); 14pp; Chinese.
XX
XX The invention relates to a method of preparation of a genetically
XX engineered vaccine for preventing and treating human breast cancer. The
XX method comprises fusing the coding gene of the Mycobacterium bovis heat
XX shock protein 65 (BCG HSP65) with the cytotoxic T lymphocyte (CTL)
XX epitope gene of MUC1 (antigen cell expressed by human breast cancer
XX cells) and the HSP65-MUC1 antigen CTL epitope is expressed in Escherichia
XX coli cells. This sequence represents DNA used in the method of the
XX invention.
XX
XX SQ Sequence 156 BP; 37 A; 42 C; 58 G; 19 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.72e-05 Length: 156
Score: 109.00 Matches: 20
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Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-057-136-1 (1-20) x ADK68635 (1-156)

Oy 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20
Db 132 GGTTCACCGCTCCGCGGCTCACGGTGTATTCTCTGCTCGGACACCGCTCGGCTCCG 73

RESULT 12
AAN90579/c
ID AAN90579 standard; cDNA; 309 BP.
XX
XX AAN90579;
XX
XX 27-AUG-2003 (revised)
XX 25-MAR-2003 (revised)
XX 04-DEC-1989 (first entry)
XX
XX pdf9.3 cDNA insert.

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XX
XX pdf9.3; human DF3 breast carcinoma-associated antigen epitope.
XX
XX Human MCF-7 breast carcinoma cells; 'ATCC HTB22'.
XX
XX WO8907107-A.
XX
XX 10-AUG-1989.
XX
XX 29-JAN-1988; 88US-00149831.
XX
XX 29-JAN-1988; 88US-00149831.
XX
XX (DANA-) DANA-FARBBER CANCER.
XX
XX Kufe DW;
XX
XX WPI; 1989-248989/34.
XX
XX P-PSDB; AAP91045, AAP91053, AAP91054, AAP90146.
XX
XX Recombinant polypeptide(s) - contains DF 3 breast carcinoma antigen
XX epitope and useful as assay reagents, and encoding DNA sequences.
XX
XX Claim 1; Fig 4; 31pp; English.
XX
XX The sequence encodes a carbohydrate-free polypeptide contg. DF3 breast
XX carcinoma antigen epitope. Useful as a competitive binding assay reagent
XX and improves diagnosis. The cDNA consists of nearly identical 60 BP
XX tandem repeats which are 85% GC-rich. See also AAP91045, AAP91046,
XX AAP91053, AAP91054. (Updated on 25-MAR-2003 to correct PA field.)
XX
XX (Updated on 27-AUG-2003 to correct OS field.)
XX
XX SQ Sequence 309 BP; 21 A; 92 C; 160 G; 36 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 3.54e-05 Length: 309
Score: 109.00 Matches: 20
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-10-057-136-1 (1-20) x AAN90579 (1-309)

Oy 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20
Db 266 GGCTCCACCGCCCCCGCCAGCCACGGGTGTCACTCGGCCCCGGACACCGCGCCCCCG 207

RESULT 13
AAD00385
ID AAD00385 standard; DNA; 525 BP.
XX
XX AAD00385;
XX
XX 29-AUG-2000 (first entry)
XX
XX Human Mucin 1 (MUC-1) protein fragment encoding DNA #2.
XX
XX Human; Mucin 1; MUC-1; tumour; pMRS30 expression vector; anti-tumour;
XX therapy; immune response; cytostatic; vaccine; ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 1..525
XX FT /*tag= a
XX FT /product= "MUC-1 protein fragment"
XX
XX WO200025827-A2.
XX
XX 11-MAY-2000.
XX
XX 18-OCT-1999; 99WO-BF007874.

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XX 30-OCT-1998; 98IT-MI002330.
XX PA (MENA ) MENARINI RICERCHE SPA.
XX PI Parente D, Di Massimo AM, De Santis R;
XX DR WPI; 2000-365410/31.
XX DR P-PSDB; AAY71021.
XX PT Composition containing one or more DNA molecules encoding fragments of a
XX PT Mucin 1 (MUC-1) protein overexpressed in tumor cells, useful in anti-
XX PT tumor therapy.
XX PS Claim 16; Fig 2; 56pp; English.
XX CC The present sequence is a DNA encoding a fragment of human Mucin 1 (MUC-
XX CC 1) antigenic protein which is overexpressed in tumour cells. The sequence
XX CC was obtained from BT20 tumour cells by reverse transcriptase- PCR and
XX CC corresponds to nucleotides 205-720 of the EMBL sequence J05581 with a
XX CC start codon and two stop codons. The present sequence is cloned into a
XX CC pMRS30 expression vector and used in pharmaceutical composition e.g.
XX CC vaccine for inducing an antigen-specific anti-tumour immune response.
XX CC Composition containing this DNA molecule is useful in anti-tumour therapy
XX CC of patients affected with tumours characterised by high MUC-1 expression
XX CC
XX SQ Sequence 525 BP; 111 A; 199 C; 128 G; 87 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6 2e-05 Length: 525
Score: 109.00 Matches: 20
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-057-136-1 (1-20) x AAD00391 (1-525)

Qy 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20
Db 256 GGAAGTACTGCTCCACACGACACGGTGTACCTCGGCTCCGGATACCAGCGCGGCCCA 315

RESULT 14
AAD00391
ID AAD00391 standard; DNA; 891 BP.
AC AAD00391;
XX 15-SEP-2003 (revised)
DT 29-AUG-2000 (first entry)
XX Ubiquitin-E. coli LacI-human Mucin 1 fusion protein encoding DNA #2.
XX DE
XX Ubiquitin; LacI; beta-galactosidase; fusion protein; human; Mucin 1;
KW MUC-1; tumour; pMRS30 expression vector; anti-tumour; therapy;
KW immune response; cytostatic; vaccine; ds.
XX OS
XX Homo sapiens.
XX OS
XX Escherichia coli.
XX OS
XX Chimeric.
XX Key Location/Qualifiers
XX FH 1..891
XX CDS /*tag= a
XX FT /product= "Ubiquitin-LacI-MUC-1 fusion protein"
XX FT misc_feature 1..369
XX FT /*tag= b
XX FT /label= UBILacI DNA
XX FT /note= "Includes ubiquitin-E. coli LacI fusion DNA"
XX FT misc_feature 370..891
XX FT /*tag= c
XX FT /note= "Human MUC-1 partial DNA that corresponds to
XX FT nucleotides 205-720 of the EMBL sequence J05581 with two

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FT stop codons"
XX WO200025827-A2.
XX PN 11-MAY-2000.
XX PD 18-OCT-1999; 99WO-EP007874.
XX PF 30-OCT-1998; 98IT-MI002330.
XX XX (MENA ) MENARINI RICERCHE SPA.
XX PA Parente D, Di Massimo AM, De Santis R;
XX PI WPI; 2000-365410/31.
XX DR P-PSDB; AAY71027.
XX DR Composition containing one or more DNA molecules encoding fragments of a
XX PT Mucin 1 (MUC-1) protein overexpressed in tumor cells, useful in anti-
XX PT tumor therapy.
XX PS Claim 18; Fig 8; 56pp; English.
XX CC The present sequence is a DNA encoding a fusion protein consisting of
XX CC human Mucin 1 (MUC-1) fragment fused to UBILacI sequence at the N
XX CC terminus. The UBILacI sequence consists of ubiquitin from MCF7 cell line
XX CC and a portion of E. coli beta-galactosidase (lacI). MUC-1 is an antigenic
XX CC protein overexpressed in tumour cells. The present sequence is cloned
XX CC into a pMRS30 expression vector and used in pharmaceutical composition
XX CC e.g. vaccine for inducing an antigen-specific anti-tumour immune
XX CC response. Composition containing this DNA molecule is useful in anti-
XX CC tumour therapy of patients affected with tumours characterised by high
XX CC MUC-1 expression. (Updated on 15-SEP-2003 to standardise OS field)
XX SQ Sequence 891 BP; 203 A; 307 C; 225 G; 156 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0.000109 Length: 891
Score: 109.00 Matches: 20
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-057-136-1 (1-20) x AAD00391 (1-891)

Qy 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20
Db 622 GGAAGTACTGCTCCACACGACACGGTGTACCTCGGCTCCGGATACCAGCGCGGCCCA 681

RESULT 15
ADI57712
ID ADI57712 standard; cDNA; 1194 BP.
XX AC ADI57712;
XX DT 22-APR-2004 (first entry)
XX DE Human breast specific nucleic acid (BSNA) #83.
XX KW Human; breast specific nucleic acid; BSNA; gene; ss; metastasis;
XX KW breast cancer; cytostatic.
XX OS Homo sapiens.
XX XX WO2003106648-A2.
XX PD 24-DEC-2003.
XX PF 16-JUN-2003; 2003WO-US018934.
XX PR 14-JUN-2002; 2002US-0389327P.
XX XX

```

Fri Jul 1 08:50:17 2005

PA	(DIAD-) DIADEXUS INC.	
XX		
PI	Salceda S, Macina RA, Turner LR, Sun Y, Liu C;	
PI		
XX		
DR	WPI: 2004-082185/08.	
DR	P-PSDB; ADI57782.	
XX		
XX		
PT	Novel isolated polypeptide comprising breast specific protein sequences,	
PT	useful for diagnosing or monitoring presence and metastases of breast	
PT	cancer in patient.	
XX		
PS	Claim 1; SEQ ID NO 83; 370pp; English.	
XX		
CC	The invention relates to human breast specific nucleic acids (BSNA) and	
CC	the breast specific proteins (BSP) they encode. The nucleic acids are	
CC	useful for determining the presence of a BSNA in a sample which involves	
CC	contacting the sample with a BSNA under conditions in which the BSNA will	
CC	selectively hybridise to a BSNA in the sample, and detecting the	
CC	hybridisation. The nucleic acids are useful for determining the presence	
CC	of a BSP in a sample which involves contacting the sample with suitable	
CC	reagent under conditions in which the reagent will selectively interact	
CC	with the BSP, and detecting the interaction of the reagent with a BSP in	
CC	the sample. The nucleic acids and proteins are useful for diagnosing or	
CC	monitoring the presence and metastases of breast cancer in a patient,	
CC	which involves determining an amount of nucleic acid or protein and	
CC	comparing the determined amount of nucleic acid or protein in the sample	
CC	of the patient to the amount of a breast specific marker in a normal	
CC	control, where a difference in the determined amount in the sample	
CC	compared to the amount in the control is associated with the presence of	
CC	breast cancer. The sequences are useful for treating a patient with	
CC	breast cancer, involving administering a composition consisting of a BSNA	
CC	or a BSP to a patient, where the administration induces an immune	
CC	response against the breast cancer cell expressing the BSNA or BSP. This	
CC	sequence represents a human BSNA of the invention.	
XX		
XX		
XX	Sequence 1194 BP: 243 A; 438 C; 275 G; 238 T; 0 U; 0 Other	
SQ		



GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 30, 2005, 06:42:59 ; Search time 2603 Seconds  
(without alignments)  
372.303 Million cell updates/sec

Title: US-10-057-136-1

Perfect score: 109

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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- 2: gb\_hg.\*
- 3: gb\_in.\*
- 4: gb\_on.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 1	109	100.0	120	6	AX192396 Sequence
C 2	109	100.0	120	6	BD000571 Human pol
3	109	100.0	525	6	BD225141 Medicinal
4	109	100.0	891	6	BD225147 Medicinal

5	109	100.0	1371	6	BD225144
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8	109	100.0	1457	6	AX959914
9	109	100.0	1737	6	BD225150
10	109	100.0	1774	6	AX959684
11	109	100.0	1774	6	AX959912
12	109	100.0	1800	6	CQ875507
13	109	100.0	1804	6	AR492318
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15	109	100.0	1804	6	HUMUCAB
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23	109	100.0	4139	6	AX334899
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28	109	100.0	4139	9	HUMANMU
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37	104	95.4	1721	6	AX335860
38	104	95.4	1721	6	AX440427
39	104	95.4	1721	6	AX587588
40	104	95.4	1721	9	HSTEYMA
41	104	95.4	1971	6	AX963157
42	104	95.4	2037	6	AX963159
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ALIGNMENTS

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LOCUS	AX192396	AX192396	AX192396.1	GI:15210363			
DEFINITION	Sequence 2 from Patent EPI103623.						
ACCESSION	AX192396						
VERSION	AX192396.1						
KEYWORDS	Homo sapiens (human)						
SOURCE	Homo sapiens						
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.						
REFERENCE	1						
AUTHORS	Taylor-Papadimitriou, J., Burchell, J. and Gendler, S.						
TITLE	Human mucin core protein: nucleic acid probes, peptide fragments and antibodies thereto, and uses thereof in diagnostic and therapeutic methods						
JOURNAL	Patent: EP 1103623-A 2 30-MAY-2001;						
FEATURES	IMPERIAL CANCER RESEARCH TECHNOLOGY LIMITED (GB)						
source	Location/Qualifiers						
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Score:

Percent Similarity: 100.00% Conservative: 0  
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US-10-057-136-1 (1-20) x AX192396 (1-120)

Qy 1 GlySerThrAlaProProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20  
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 Db 87 GGCTCCACCGCCCCCGACCCACGGTGTACCTCGGCCCGGACACAGCGCGGCCCG 28

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 LOCUS BD000571 120 bp DNA linear PAT 31-JAN-2002  
 DEFINITION Human polymorphic epithelial mucin core protein and nucleic acid  
 encoding the protein.

ACCESSION BD000571  
 VERSION BD000571.1 GI:18623684  
 KEYWORDS JP 2000333675-A/2.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 120)  
 AUTHORS Papadimitrov J.T., Jendora, S. and Bachieru, J.  
 TITLE Human polymorphic epithelial mucin core protein and nucleic acid  
 encoding the protein  
 JOURNAL Patent: JP 2000333675-A 2 05-DEC-2000;  
 IMPERIAL CANCER RESEARCH TECHNOLOGY LTD  
 COMMENT OS Homo sapiens (human)  
 PN JP 2000333675-A/2  
 PD 05-DEC-2000  
 PF 26-APR-2000 JP 2000125724  
 PR 07-JAN-1987 GB 8700269, 07-JAN-1987 GB 8700279 PR  
 22-APR-1987 US 041306, 09-NOV-1987 GB 8726172 PI JOYCE  
 TAYLOR PAPADIMITROV, SANDRA JENDORA, JOY BACHIERU PC  
 C12N15/02, A61K38/00, A61K39/395, A61K49/00, A61P35/00, PC  
 C07K14/47,  
 PC C07K16/44, C12N5/10, C12P21/08// (C12N15/02, C12R1:91), (C12N5/10,  
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US-10-057-136-1 (1-20) x BD000571 (1-120)

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RESULT 3  
 BD225141  
 LOCUS BD225141 525 bp DNA linear PAT 17-JUL-2003  
 DEFINITION Medicinal composition having antitumor effect and containing DNA  
 encoding antigenic protein.  
 ACCESSION BD225141

BD225141.1 GI:33034911  
 JP 2002528519-A/2.  
 Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 525)  
 AUTHORS Pallante, D., Massimo, A.M.D. and Desantis, R.  
 TITLE Medicinal composition having antitumor effect and containing DNA  
 encoding antigenic protein  
 JOURNAL Patent: JP 2002528519-A 2 03-SEP-2002;  
 MENARINI RICERCHE SPA  
 COMMENT OS Homo sapiens (human)  
 PN JP 2002528519-A/2  
 PD 03-SEP-2002  
 PF 18-OCT-1999 JP 2000579265  
 PR 30-OCT-1998 IT MI98A002330  
 PI DINO PALLENTI, ANNA MARIA D MASSIMO, RITA DESANTIS PC  
 A61K38/00, A61K35/76, A61K39/00, A61K48/00, A61P35/00, C12N15/09, PC  
 A61K37/02,  
 PC C12N15/00  
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 DNA encoding  
 CC antigenic protein  
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FEATURES  
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 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 6 Gaps:

US-10-057-136-1 (1-20) x BD225141 (1-525)

Qy 1 GlySerThrAlaProProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20  
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 Db 256 GGAAGTACTGCTCCACGACACACGGTGTACCTCGGCTCCGATACACGCGCGGCCCA 315

RESULT 4  
 BD225147  
 LOCUS BD225147 891 bp DNA linear PAT 17-JUL-2003  
 DEFINITION Medicinal composition having antitumor effect and containing DNA  
 encoding antigenic protein.  
 ACCESSION BD225147  
 VERSION BD225147.1 GI:33034917  
 KEYWORDS JP 2002528519-A/8.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 891)  
 AUTHORS Pallante, D., Massimo, A.M.D. and Desantis, R.  
 TITLE Medicinal composition having antitumor effect and containing DNA  
 encoding antigenic protein  
 JOURNAL Patent: JP 2002528519-A 8 03-SEP-2002;  
 MENARINI RICERCHE SPA  
 COMMENT OS Homo sapiens (human)  
 PN JP 2002528519-A/8  
 PD 03-SEP-2002  
 PF 18-OCT-1999 JP 2000579265  
 PR 30-OCT-1998 IT MI98A002330  
 PI DINO PALLENTI, ANNA MARIA D MASSIMO, RITA DESANTIS PC  
 A61K38/00, A61K35/76, A61K39/00, A61K48/00, A61P35/00, C12N15/09, PC

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A61K37/02.
PC C12N15/00
CC Medicinal composition having antitumor effect and containing
CC DNA encoding
CC antigenic protein
FH Key Location/Qualifiers
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FT Location/Qualifiers
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FEATURES
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Alignment Scores:
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Score: 109.00 Matches: 20
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-057-136-1 (1-20) x BD225147 (1-891)

Qy 1 GlySerThrAlaProProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20
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Db 622 GGAAGTACTGCTCCACGACACACGGTGTACCTCGGCTCCGGATACCGAGCGCGGCCCA 681

RESULT 5
LOCUS BD225144 1371 bp DNA linear PAT 17-JUL-2003
DEFINITION Medicinal composition having antitumor effect and containing DNA
encoding antigenic protein.
ACCESSION BD225144
VERSION BD225144.1 GI:33034914
KEYWORDS JP 2002528519-A/5.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1371)
AUTHORS Pallente,D., Massimo,A.M.D. and Desantis,R.
TITLE Medicinal composition having antitumor effect and containing DNA
encoding antigenic protein
JOURNAL Patent: JP 2002528519-A 5 03-SEP-2002;
MENARINI RICERCHE SPA
COMMENT OS Homo sapiens (human)
PN JP 2002528519-A/5
PD 03-SEP-2002
PF 18-OCT-1999 JP 2000579265
PI 30-OCT-1998 IT MI98A002330
PI DINO PALLENTE,ANNA MARIA D MASSIMO,RITA DESANTIS PC
A61K38/00,A61K35/76,A61K39/00,A61K48/00,A61P35/00,C12N15/09, PC
A61K37/02,
PC C12N15/00
CC Medicinal composition having antitumor effect and containing
CC DNA encoding
CC antigenic protein
FH Key Location/Qualifiers
FT source 1..1371 /organism='Homo sapiens (human)'.
FT Location/Qualifiers
1..1371
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/mol_type='genomic DNA'
/db_xref='taxon:9606'

FEATURES
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ORIGIN
Alignment Scores:
Pred. No.: 0.00113 Length: 1371
Score: 109.00 Matches: 20
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 0 Gaps: 0
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-057-136-1 (1-20) x BD225144 (1-1371)

Qy 1 GlySerThrAlaProProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20
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Db 325 GGAAGTACCCTCCACGACACACGGTGTACCTCGGCTCCGGATACCGAGCGCGGCCCA 384

RESULT 6
LOCUS AF423031 1414 bp mRNA linear SYN 10-JUL-2003
DEFINITION Synthetic construct Homo sapiens mucin variant MUC1-CT58 (MUC1)
mRNA, complete cds; alternatively spliced.
ACCESSION AF423031
VERSION AF423031.1 GI:19338621
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 1414)
AUTHORS Hinojosa-Kurtzberg,A.M., Johansson,M.E., Madsen,C.S., Hansson,G.C.
and Gendler,S.J.
TITLE Novel MUC1 splice variants contribute to mucin overexpression in
CFTR-deficient mice
JOURNAL Am. J. Physiol. Gastrointest. Liver Physiol. 284 (5), G853-G862
(2003)
MEDLINE 22570517
PUBMED 12529261
REFERENCE 2 (bases 1 to 1414)
AUTHORS Hinojosa-Kurtzberg,A.M. and Gendler,S.J.
TITLE Direct Submission
JOURNAL Submitted (21-SEP-2001) Biochemistry, Mayo Clinic, 13400 E. Shea
Boulevard, Scottsdale, AZ 85259, USA
FEATURES
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/organism='synthetic construct'
/mol_type='mRNA'
/db_xref='taxon:32630'
/note='Homo sapiens gene in transgenic Mus musculus
C57BL/6; isolated from intestinal mucosa'
1..1414
/gene='MUC1'
1..1386
/gene='MUC1'
/note='alternatively spliced; contains exon 6b resulting
in variant carboxy-terminal domain; lacks sites for
beta-catenin and Grb2 interactions; derived from Homo
sapiens'
/codon_start=1
/transl_table=11
/product='mucin variant MUC1-CT58'
/protein_id='AAU86735.1'
/db_xref='GI:19338622'
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VPTSTENKAVMTSSVLSHSPGSGSTTQGDVTLAPATEPASGSAATWQDVTSP
VTRPALGTTTPPAHDVTAPDNKPAAGTAPPAHGTVPADTRPAGSTAPPAHGVTS
APDNRPALGSTAPPVHNTVSAGSAGSASTLVHNGTSARATTPASKSTPFIPISSH
SDPTTLASHSTKTDASTHSTVPTLTSSNHSSTPOLSTCVSPFLLSFLSNLQFNS
SLEDPTDYIQELQDISEMFLQIKQGGFLGSLNIXKRPQGVVVQLTLAPREGTINV
HDEVTQFNQKTEAASNYLITSDVSVDPFPPFSAQSGAGVPGWGLALLVLCVLA
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KEWRVDRERLA"

ORIGIN
Alignment Scores:
Pred. No.: 0.00116 Length: 1414
Score: 109.00 Matches: 20
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0
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Qy 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20
Db 385 GGCTCCACCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCG 444

RESULT 7
LOCUS CQ715242 1455 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 1176 from Patent WO02068579.
ACCESSION CQ715242
VERSION CQ715242.1 GI:42276099
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
TITLE Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
thereof
JOURNAL Patent: WO 02068579-A 1176 06-SEP-2002;
PE Corporation (NY) (US)
FEATURES
source
location/Qualifiers
1..1455
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores:
Pred. No.: 0.00119 Length: 1455
Score: 109.00 Matches: 20
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-057-136-1 (1-20) x CQ715242 (1-1455)

Qy 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20
Db 412 GGCTCCACCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCG 471

RESULT 8
LOCUS AX959914 1457 bp DNA linear PAT 14-JAN-2004
DEFINITION Sequence 19 from Patent WO03100060.
ACCESSION AX959914
VERSION AX959914.1 GI:40880143
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Burden, N.G., Ellis, J.H. and Hamblin, P.A.
TITLE Muc-1 antigen with reduced number of vnter repeat units
JOURNAL Patent: WO 03100060-A 19 04-DEC-2003;
GLAXO GROUP LIMITED (GB)
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location/Qualifiers
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/mol_type="unassigned DNA"
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ORIGIN
Alignment Scores:
Pred. No.: 0.00119 Length: 1457
Score: 109.00 Matches: 20
Percent Similarity: 100.00% Conservative: 0

US-10-057-136-1 (1-20) x AX959914 (1-1457)

Qy 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20
Db 403 GGCTCCACCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCG 462

RESULT 9
LOCUS BD225150 1737 bp DNA linear PAT 17-JUL-2003
DEFINITION Medicinal composition having antitumor effect and containing DNA
encoding antigenic protein.
ACCESSION BD225150
VERSION BD225150.1 GI:33034920
KEYWORDS JP 2002528519-A/11.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1737)
AUTHORS Pallente, D., Massimo, A.M.D. and Desantis, R.
TITLE Medicinal composition having antitumor effect and containing DNA
encoding antigenic protein
JOURNAL Patent: JP 2002528519-A 11 03-SEP-2002;
MENARINI RICERCHE SPA
COMMENT OS Homo sapiens (human)
PN JP 2002528519-A/11
PD 03-SEP-2002
PF 18-OCT-1999 JP 2000579265
PR 30-OCT-1998 IT MI98A002330
PI DINO PALLENTI, ANNA MARIA D MASSIMO, RITA DESANTIS PC
A61K38/00, A61K35/76, A61K39/00, A61K48/00, A61P35/00, C12N15/09, PC
A61K37/02,
PC C12N15/00
CC Medicinal composition having antitumor effect and containing
antigenic protein
FH Key Location/Qualifiers
FT source 1..1737
/organism="Homo sapiens (human)"

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Alignment Scores:
Pred. No.: 0.00139 Length: 1737
Score: 109.00 Matches: 20
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-057-136-1 (1-20) x BD225150 (1-1737)

Qy 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20
Db 691 GGAAGTACCCTCCACGACACACGGTGTACCTCGGTCGCGATACGAGCCGCGCCCA 750

RESULT 10
LOCUS AX959684 1774 bp DNA linear PAT 14-JAN-2004
DEFINITION Sequence 10 from Patent WO03099193.
ACCESSION AX959684
VERSION AX959684.1 GI:40880030
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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RESULT 12					
CQ875507					
LOCUS	CQ875507	1800 bp	DNA	linear	PAT 27-SEP-2004
DEFINITION	Sequence 16 from Patent WO2004076665..				
ACCESSION	CQ875507				
VERSION	CQ875507.1	GI:52748471			
KEYWORDS	.				
SOURCE	synthetic construct				

REFERENCE 1 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
AUTHORS Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,  
Horrikan, S., Soppet, D.R. and Weaver, Z.  
TITLE Cancer gene determination and therapeutic screening using signature  
gene sets

JOURNAL Patent: WO 0194629-A 5876 13-DEC-2001;

FEATURES Avalon Pharmaceuticals (US)

source Location/Qualifiers  
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/db\_xref="taxon:9606"

## ORIGIN

Alignment Scores:  
Pred. No.: 0.00144 Length: 1804  
Score: 109.00 Matches: 20  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-057-136-1 (1-20) x AX335367 (1-1804)

Qy 1 GlySerThrAlaProProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20  
Db 457 GGCTCCACCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCG 516

## RESULT 15

HUMMUCAB 1804 bp mRNA linear PRI 07-JAN-1995  
LOCUS Human polymorphic epithelial mucin (PEM) mRNA, complete cds.

DEFINITION J05581  
ACCESSION J05581  
VERSION J05581.1 GI:188869  
KEYWORDS polymorphic epithelial mucin.  
SOURCE Homo sapiens (human)

## ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 1804)  
AUTHORS Gendler, S.J., Lancaster, C.A., Taylor-Papadimitriou, J., Duhig, T.,  
Peat, N., Burchell, J., Pemberton, L., Lalani, E.N. and Wilson, D.  
TITLE Molecular cloning and expression of human tumor-associated  
polymorphic epithelial mucin

J. Biol. Chem. 265 (25), 15286-15293 (1990)

J05581

90368715

1697589

Original source text: Homo sapiens adult adenocarcinoma cDNA to

mRNA.

Draft entry and computer-readable sequence for [J. Biol. Chem.

(1990) In press] kindly submitted

by S.J. Gendler, 26-JUN-1990.

FEATURES Location/Qualifiers

## source

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/tissue\_type="adenocarcinoma"  
/dev\_stage="adult"  
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/gene="MCNAA"  
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73..1500  
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/protein\_id="AAA59876.1"  
/db\_xref="GI:188870"

## gene

## mRNA

## CDS

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VTPPALGSTTPPAHDVTSAPDNKPAKSTAPAHGVTSAEDTRPAKSTAPAHGVTSA  
APDNKPAKSTAPAHGVTSAEDTRPAKSTAPAHGVTSAEDTRPAKSTAPAHGVTSA  
SDPTTLASHSTTKTDASSTHSTVPLTSSNHSSTPOLSTGVSTGVSFFLSPHISNLOFNS  
SLDDPTDYQELQDRISEMPLQIYKGGFLGSLNFKRFGSVVQTLTAPFREGTINVA  
HDVETQFNQYQTEAASRYNLTISDVSVSDVFPFSAQSAGVPCWGLALVLVCVLVA  
LAIVYLIALAVCCCRKNYGOLDIFPARDTYHPMSEYPTVTHGRVYVPPSSTDRSPYE  
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sig\_peptide

/gene="MCNAA"

mat\_peptide

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/gene="MCNAA"

/product="polymorphic epithelial mucin"

1783..1788

/gene="MCNAA"

## ORIGIN

Alignment Scores:

Pred. No.: 0.00144 Length: 1804  
Score: 109.00 Matches: 20  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-10-057-136-1 (1-20) x HUMMUCAB (1-1804)

Qy 1 GlySerThrAlaProProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20  
Db 457 GGCTCCACCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCG 516

Search completed: June 30, 2005, 08:01:32

Job time : 2608 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 30, 2005, 05:41:13 ; Search time 345 Seconds  
(without alignments)  
29.686 Million cell updates/sec

Title: US-10-057-136-1

Perfect score: 109

Sequence: 1 GSTAPPAHGVTISAPDTRPAP 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	109	100.0	1255	1 MUC1_HUMAN	P15941 h mucin 1 p
2	94	86.2	475	1 MUC1_HYLLA	Q29435 hylobates 1
3	93	85.3	256	2 Q7M4M7	Q7m4m7 homo sapien
4	74	67.9	553	2 Q9MZL1	Q9mzl1 macaca mula
5	68	62.4	20	2 Q9UMI8	Q9umi8 homo sapien
6	59	54.1	745	2 Q9XU06	Q8x06 bradyrhizob
7	58.5	53.7	1334	2 Q9RKR9	Q9rkr9 streptomyce
8	56	51.4	779	2 Q6FTP1	Q6ftpl candida gla
9	56	51.4	933	2 Q8M2Z6	Q8mz26 homo sapien
10	55	50.5	933	2 Q9ULK3	Q9ulk3 homo sapien
11	55	50.5	1339	2 Q6UX35	Q6ux35 homo sapien
12	54	49.5	276	2 Q81YJ0	Q81yj0 homo sapien
13	54	49.5	282	2 Q95K74	Q95k74 macaca fasc
14	54	49.5	282	2 Q9N088	Q9n088 macaca fasc
15	54	49.5	290	2 Q6ESR4	Q6esr4 oryza sativ
16	54	49.5	403	2 Q42417	Q42417 gallus gall
17	54	49.5	558	2 Q82IR8	Q82ir8 streptomyce
18	54	49.5	628	1 ASH2_HUMAN	Q9ub13 homo sapien
19	54	49.5	705	2 Q7SFFN5	Q7sfn5 mycobacteri
20	54	49.5	355	2 Q73ZH6	Q73zh6 mycobacteri
21	53	48.6	584	2 Q8XZC6	Q8xzc6 ralstonia s
22	53	48.6	673	2 Q8V725	Q8v725 cercopithec
23	53	48.6	673	2 Q7T5C3	Q7t5c3 cercopithec
24	53	48.6	823	2 Q6DKA9	Q6dka9 xenopus lae
25	53	48.6	823	2 Q82E38	Q82e38 streptomyce
26	52	47.7	157	2 Q7W0D8	Q7w0d8 bordetella
27	52	47.7	188	2 Q8Z690	Q8z690 salmonella
28	52	47.7	244	2 Q8ZP19	Q8zpl9 salmonella
29	52	47.7	360	2 Q7QJ16	Q7qj16 anopheles g
30	52	47.7	406	2 Q8VPM8	Q8vpm8 micrococcus
31	52	47.7			

32 52 47.7 561 2 Q6PK46 Q6pk46 homo sapien  
33 52 47.7 568 2 Q7TSC9 Q7tsc9 mus musculus  
34 52 47.7 632 1 P021\_RAT P31503 rattus norv  
35 52 47.7 650 2 Q7TSD0 Q7tsd0 mus musculus  
36 52 47.7 739 1 P021\_CHICK P15143 gallus gall  
37 52 47.7 743 1 P021\_HUMAN P14859 homo sapien  
38 52 47.7 745 1 P021\_PIG Q29076 sus scrofa  
39 52 47.7 770 1 P021\_MOUSE P25425 mus musculus  
40 52 47.7 793 2 Q8BT04 Q8bt04 mus musculus  
41 52 47.7 901 2 Q7SD01 Q7sd01 neurospora  
42 51 46.8 130 2 Q9ZXJ0 Q9zxj0 bacterioph  
43 51 46.8 241 2 Q8YQJ7 Q8yqj7 anabaena sp  
44 51 46.8 256 2 Q8Y3A4 Q8y3a4 ralstonia s  
45 51 46.8 377 2 Q9Z4X8 Q9z4x8 streptomyce

#### ALIGNMENTS

RESULT 1  
MUC1\_HUMAN  
ID MUC1\_HUMAN STANDARD; PRT; 1255 AA.  
AC P15941; P13931; P15942; P17626; Q14128; Q14876; Q16437; Q16442;  
AC Q16615; Q9BXA4; Q9UE75; Q9UE76; Q9UQL1; Q9V4J2;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Mucin 1 precursor (MUC-1) (Polymorphic epithelial mucin) (PEM) (PEMT)  
DE (Episialin) (Tumor-associated mucin) (Carcinoma-associated mucin)  
DE (Tumor-associated epithelial membrane antigen) (EMA) (H23AG) (Peanut-  
DE reactive urinary mucin) (PUM) (Breast carcinoma-associated antigen  
DE DF3) (CD227 antigen).  
GN Name=MUC1;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBT\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RC TISSUE=Pancreas;  
RX MEDLINE=90368716; PubMed=2394722;  
RA Lan M.S., Batra S.K., Qi W.-N., Metzgar R.S., Hollingsworth M.A.;  
RL "Cloning and sequencing of a human pancreatic tumor mucin cDNA.";  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
RX MEDLINE=90202794; PubMed=2318825;  
RA Lichtenberg M.J.L., Vos H.L., Gennissen A.M.C., Hilkens J.;  
RL "Episialin, a carcinoma-associated mucin, is generated by a  
RT polymorphic gene encoding splice variants with alternative amino  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RC TISSUE=Breast carcinoma;  
RX MEDLINE=90368715; PubMed=1697589;  
RA Gendler S.J., Lancaster C.A., Taylor-Papadimitriou J., Duhig T.,  
RA Peat N., Burchell J., Pemberton L., Lalani E.-N., Wilson D.;  
RT "Molecular cloning and expression of human tumor-associated  
RN [4]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RC MEDLINE=91097524; PubMed=2268309;  
RA Lancaster C.A., Peat N., Duhig T., Wilson D., Taylor-Papadimitriou J.,  
RA Gendler S.J.;  
RT "Structure and expression of the human polymorphic epithelial mucin  
RN [5]  
RP SEQUENCE FROM N.A. (ISOFORM 5).  
RC TISSUE=Breast carcinoma;  
RX MEDLINE=90276413; PubMed=2351132;





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RN [24]
RP PHOSPHORYLATION.

Query Match 100.0%; Score 109; DB 1; Length 1255;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSTAPPAHGVTSAAPDTRAP.20
Db 129 GSTAPPAHGVTSAAPDTRAP 148

RESULT 2
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AC Q29435;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Mucin 1 precursor (MUC-1).
GN Name=MUC1;
OS Hylobates lar (Common gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=9580;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96351712; PubMed=8747930;
RA Spicer A.P., Dubig T., Chilton B.S., Gendler S.J.;
RT "Analysis of mammalian MUC1 genes reveals potential functionally
RL Mamm. Genome 6:885-888(1995).
CC -!- FUNCTION: Direct or indirect interaction with actin cytoskeleton
CC (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- PTM: Highly O-glycosylated and probably also N-glycosylated.
CC -!- SIMILARITY: Contains 1 SEA domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L41589; AAA69965.1; -
DR EMBL; L41625; AAA69918.1; -
DR EMBL; L41624; AAA69918.1; JOINED.
DR InterPro; IPR000082; SEA.
DR Pfam; PF01390; SEA; 1.
DR SMART; SM00200; SEA; 1.
DR PROSITE; PS50024; SEA; 1.
KW Actin-binding; Cytoskeleton; Glycoprotein; Repeat; Signal;
FT SIGNAL 1 23 Potential.
FT CHAIN 24 475 Mucin 1.
FT DOMAIN 24 380 Extracellular (Potential).
FT TRANSMEM 381 401 Potential.
FT DOMAIN 402 475 Cytoplasmic (Potential).
FT REPEAT 102 121 1.
FT REPEAT 122 141 2.
FT REPEAT 142 161 3.
FT REPEAT 162 181 4.
FT DOMAIN 254 371 SEA.
SQ SEQUENCE 475 AA; 49371 MW; D7A699D6D68C6622 CRC64;

Query Match 86.2%; Score 94; DB 1; Length 475;
Best Local Similarity 94.4%; Pred. No. 0.00037;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GSTAPPAHGVTSAAPDTRP 18
Db 129 GSTAPPAHGVTSAAPDTRP 148

RESULT 3
Q7M4M7 PRELIMINARY; PRT; 256 AA.
AC Q7M4M7;
DT 01-MAR-2004 (TrEMBLrel.. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Tumor-associated antigen DF3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90058554; PubMed=2582438;
RA Merlo G.R., Siddiqui J., Cropp C.S., Liscia D.S., Lidereau R.,
RA Callahan R., Kufe D.W.;
RT "Frequent alteration of the DF3 tumor-associated antigen gene in
RL Cancer Res. 49:6966-6971(1989).
DR PIR; A60533; A60533.
DR GO; GO:0005198; P:structural molecule activity; IEA.
DR GO; GO:0019088; P:virial assembly; IEA.
DR InterPro; IPR000982; Matrix.
DR PRODOM; PD000741; Matrix; 2.
SQ SEQUENCE 256 AA; 25766 MW; E0430F0BA7F30B04 CRC64;

Query Match 85.3%; Score 93; DB 2; Length 256;
Best Local Similarity 85.0%; Pred. No. 0.00027;
Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GSTAPPAHGVTSAAPDTRAP 20
Db 12 GSTAPPAHGVTSAAPDTRAP 31

RESULT 4
Q9MZL1 PRELIMINARY; PRT; 553 AA.
AC Q9MZL1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mucin 1 (Fragment).
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20330533; PubMed=10869775; DOI=10.1016/S0264-410X(00)00143-2;
RA Vaughan H.A., Ho D.W.M., Karanikas V., Sandrin M.S., McKenzie I.F.C.,
RA Pietersz G.A.;
RT "The immune response of mice and cynomolgus monkeys to macaque mucin
RT 1-mannan".
RL Vaccine 18:3297-3309(2000).
DR EMBL; AF176947; AAF82403.1; -
DR InterPro; IPR000082; SEA.
DR Pfam; PF01390; SEA; 1.
DR SMART; SM00200; SEA; 1.
DR PROSITE; PS50024; SEA; 1.
FT NON TER 1 1
FT NON TER 553 553
SQ SEQUENCE 553 AA; 55778 MW; 6D7E6DD2EE929318 CRC64;

Query Match 67.9%; Score 74; DB 2; Length 553;
Best Local Similarity 75.0%; Pred. No. 0.18;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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QY 1 GSTAPPAGHGVTSAPDTRPAP 20
DB 107 GSTGPPARVVTISAPDTSAP 126

RESULT 5
Q9UMI8 PRELIMINARY; PRT; 20 AA.
AC Q9UMI8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Mucin (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89235154; PubMed=2715633;
RA Xing P.X., Tjandra J.J., Reynolds K., McLaughlin P.J., Purcell D.F.J.,
RA McKenzie I.F.C.;
RT "Reactivity of anti-human milk fat globule antibodies with synthetic
RL peptides."
DR EMBL; M26316; AAA36336.1; -.
DR PIR; S10571; S10571.
FT NON_TER 1
FT NON_TER 20
SQ SEQUENCE 20 AA; 1887 MW; 5B3473EABFAD87 CRC64;

Query Match 62.4%; Score 68; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSTAPPAGHGVTS 13
DB 8 GSTAPPAGHGVTS 20

RESULT 6
Q89X06 PRELIMINARY; PRT; 745 AA.
AC Q89X06;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Blr0521 protein.
GN OrderedLocusNames=blr0521;
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Bradyrhizobium.
OX NCBI_TaxID=375;
RN [1]
RP SEQUENCE FROM N.A.
RX STAFIN=USDA110;
RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
RA Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
RA Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
RA Tabata S.;
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
RT Bradyrhizobium japonicum USDA110."
RL DNA Rep. 9:189-197(2002).
DR EMBL; AP005936; BAC45786.1; -.
DR HSSP; P07176; 1OAP.
DR GO; GO:0009279; C:outer membrane (sensu Gram-negative Bacteria); IEA.
DR GO; GO:0005199; F:structural constituent of cell wall; IEA.
DR InterPro; IPR006665; OmpA/MotB.
DR InterPro; IPR003882; PstII_extensin.
DR Pfam; PF00691; OmpA; 1.
DR PRINTS; PR01218; PSTLEXTENSIN.
DR ProDom; PD000930; OmpA/MotB; 1.

KW Complete proteome.
SQ SEQUENCE 745 AA; 74544 MW; 155BDFCC74DBC6D CRC64;

Query Match 54.1%; Score 59; DB 2; Length 745;
Best Local Similarity 64.7%; Pred. No. 22;
Matches 11; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 4 APPAGHGVTSAPDTRPAP 20
DB 269 SPPAGATPAPTTTAP 285

RESULT 7
Q9RKR9 PRELIMINARY; PRT; 1334 AA.
AC Q9RKR9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative multi-domain regulatory protein.
GN ORFNames=SC75A.05c;
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=A3(2) / M145;
RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper A., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neill S.,
RA Rabinowitsch E., Rajandream M.A., Rutherford K.M., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
DR EMBL; AL939112; CAB61705.1; -.
DR PIR; T50568; T50568.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0000156; F:two-component response regulator activity; IEA.
DR GO; GO:0042829; P:defense response to pathogen; IEA.
DR GO; GO:0000160; P:two-component signal transduction system (p. .; IEA.
DR InterPro; IPR009059; bi_resp_regltr_C.
DR InterPro; IPR005158; BTAD.
DR InterPro; IPR000767; Disease resist.
DR InterPro; IPR008941; TPR-like.
DR InterPro; IPR001867; Trans_reg_C.
DR Pfam; PF03704; BTAD; 1.
DR Pfam; PF00486; Trans_reg_C; 1.
DR PRINTS; PR00364; DISEASERSIST.
DR ProDom; PD000329; Trans_reg_C; 1.
KW Complete proteome.
SQ SEQUENCE 1334 AA; 138786 MW; 78DC746883B8778C CRC64;

Query Match 53.7%; Score 58.5; DB 2; Length 1334;
Best Local Similarity 68.4%; Pred. No. 45;
Matches 13; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 2 STAPPAGHGVTSAPDTRPAP 20
DB 328 STAPP-HDTASAADTAP 345

RESULT 8
Q8X1F0 PRELIMINARY; PRT; 654 AA.
ID Q8X1F0
AC Q8X1F0;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)

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DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)  
 DE 01-MAR-2004 (TReMBLrel. 26, Last annotation update)  
 DE PAKI kinase.  
 OS Cryptococcus neoformans var. neoformans.  
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;  
 OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.  
 OC NCBI\_TaxID=40410;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE=22343357; PubMed=12455960; DOI=10.1128/EC.1.2.257-272.2002;  
 RA Wang P., Nichols C.B., Lengeler K.B., Cardenas M.B., Cox G.M.,  
 RA Perfect J.R., Heitman J.;  
 RA "Mating-type-specific and nonspecific PAK kinases play shared and  
 RT divergent roles in Cryptococcus neoformans.";  
 RL Eukaryotic Cell 1:257-272(2002).  
 RN [2]  
 RN SEQUENCE FROM N.A.  
 RP Breeding C.S., Lengeler K.B., Wang P., Heitman J.;  
 RA Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
 CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
 DR EMBL; AF391151; AAL58842.1; -;  
 DR HSSP; Q13153; IF3M.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
 DR GO; GO:0016740; F:transferase activity; IEA.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR Pfam; PF00786; PBD; 1.  
 DR Pfam; PF00069; Pkinase; 1.  
 DR ProDom; PD000001; Prot kinase; 1.  
 DR SMART; SM00285; PBD; 1\_  
 DR SMART; SM00220; S\_TKC; 1.  
 DR PROSITE; PS0108; CRIB; 1.  
 DR PROSITE; PS0107; PROTEIN KINASE ATP; UNKNOWN\_1.  
 DR PROSITE; PS0011; PROTEIN KINASE DOM; 1.  
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.  
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.  
 SQ SEQUENCE 654 AA; 71267 MW; DCEPAL6A54FB9215 CRC64;

Query Match 51.4%; Score 56; DB 2; Length 654;  
 Best Local Similarity 62.5%; Pred. No. 47;  
 Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 5 PPAHGVTSAPDTRAP 20  
 ||| :||| |||  
 Db 251 PPHPTSSAPPTAPAP 266

RESULT 9  
 Q6FTP1 PRELIMINARY; PRT; 779 AA.  
 AC Q6FTP1  
 DT 05-JUL-2004 (TReMBLrel. 27, Created)  
 DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)  
 DE Similar to sp|P37370 Saccharomyces cerevisiae YLR337c VRP1.  
 GN ORFNames=CAGL0G00968g;  
 OS Candida glabrata CBS138.  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; mitosporic Saccharomycetales; Candida.  
 OC NCBI\_TaxID=284593;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=CBS138;  
 RC Genolevures;  
 RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,  
 RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talia E.,  
 RA Goffard N., Frangul L., Aigle M., Anthouard V., Babour A., Barbe V.,  
 RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,  
 RA Boissrame A., Boyer J., Cattolico L., Confanioli F., de Daruvar A.,  
 RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,  
 RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,  
 RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,  
 RA Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,

RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,  
 RA Swennene D., Tekala F., Wesolowski-Louvel M., Weschof E., Wirth B.,  
 RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,  
 RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,  
 RA Wincker P., Souciet J.L.;  
 RT "Genome evolution in yeasts.";  
 RL Nature 430:35-44(2004).  
 DR EMBL; CR380953; CAG59330.1; -;  
 DR InterPro; IPR003124; WH2.  
 DR Pfam; PF02205; WH2; 2.  
 DR SMART; SM00246; WH2; 2.  
 SQ SEQUENCE 779 AA; 75743 MW; CB50564FBF43156E CRC64;

Query Match 51.4%; Score 56; DB 2; Length 779;  
 Best Local Similarity 64.7%; Pred. No. 56;  
 Matches 11; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 4 APPAHGVTSAPDTRAP 20  
 ||| :||| |||  
 Db 419 APPAPMTSAPPAPPPAP 435

RESULT 10  
 Q6MZZ6 PRELIMINARY; PRT; 933 AA.  
 ID Q6MZZ6  
 AC Q6MZZ6  
 DT 05-JUL-2004 (TReMBLrel. 27, Created)  
 DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)  
 DE Hypothetical protein DKFZp686E0469.  
 GN Name=DKFZp686E0469;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RP TISSUE=Human endometrium carcinoma cell line;  
 RC The German Human cDNA Consortium;  
 RA Ansorge W., Krieger S., Regiert T., Rittmueller C., Schwager B.,  
 RA Mewes H.W., Weil B., Amid C., Oeanger A., Fobo G., Han M., Wiemann S.;  
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BX640796; CAE45879.1; -;  
 KW Hypothetical protein.  
 SQ SEQUENCE 933 AA; 102860 MW; 188A7B37EC94669B CRC64;

Query Match 50.5%; Score 55; DB 2; Length 933;  
 Best Local Similarity 45.0%; Pred. No. 90;  
 Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 1 GSTAPPAHGVTSAPDTRAP 20  
 ||| :||| |||  
 Db 19 GSTAHPHPAIPNSPPSTFVP 38

RESULT 11  
 Q9ULK3 PRELIMINARY; PRT; 1339 AA.  
 ID Q9ULK3  
 AC Q9ULK3  
 DT 01-MAY-2000 (TReMBLrel. 13, Created)  
 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)  
 DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)  
 DE KIAA1217 protein (Fragment).  
 GN Name=KIAA1217;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RP TISSUE=Brain;  
 RC MEDLINE=20039619; PubMed=10574462;  
 RA Nagase T., Ishikawa K., Kikuno R., Hiroseawa M., Nomura N., Ohara O.;

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RT "Prediction of the coding sequences of unidentified human genes. XV.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro.";
RL DNA Res. 6:337-345(1999).
DR EMBL; AB033043; BAA86531.2; -.
FT NON TPR
SQ SEQUENCE 1339 AA; 146176 MW; 474485053148A56 CRC64;

Query Match 50.5%; Score 55; DB 2; Length 1339;
Best Local Similarity 45.0%; Pred. No. 1.3e+02;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 1 GSTAPPAGHGVTSAPDTRPAP 20
Db 296 GSTAPPAPHPAIPNSPSPFPVP 315
||||| : : : : :

RESULT 12
Q6UX35 PRELIMINARY; PRT; 276 AA.
AC Q6UX35;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE ESRM828.
GN ORFNames=UNQ828;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
DR EMBL; AY358534; AAQ88898.1; -.
SQ SEQUENCE 276 AA; 29426 MW; 72C81C7DF9B7CB89 CRC64;

Query Match 49.5%; Score 54; DB 2; Length 276;
Best Local Similarity 62.5%; Pred. No. 36;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 5 PPAHGVTSPDTRPAP 20
Db 27 PPAQSSSPRTPPAP 42
||||| : : : : :

RESULT 13
Q81YJ0 PRELIMINARY; PRT; 282 AA.
AC Q81YJ0;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein DKFZp547D2210.
GN Name=DKFZp547D2210;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

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RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Saplenton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC035736; AAH35736.1; -.
KW Hypothetical protein.
SQ SEQUENCE 282 AA; 30076 MW; 772F37069CB472C8 CRC64;

Query Match 49.5%; Score 54; DB 2; Length 282;
Best Local Similarity 62.5%; Pred. No. 36;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 5 PPAHGVTSPDTRPAP 20
Db 27 PPAQSSSPRTPPAP 42
||||| : : : : :

RESULT 14
Q95K74 PRELIMINARY; PRT; 282 AA.
AC Q95K74;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Temporal lobe right;
RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
RA Suzuki Y., Sugano S., Hashimoto K.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB063097; BAB60803.1; -.
KW Hypothetical protein.
SQ SEQUENCE 282 AA; 30076 MW; 772F37069CB472C8 CRC64;

Query Match 49.5%; Score 54; DB 2; Length 282;
Best Local Similarity 62.5%; Pred. No. 36;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 5 PPAHGVTSPDTRPAP 20
Db 27 PPAQSSSPRTPPAP 42
||||| : : : : :

RESULT 15

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Q9N088  
 ID Q9N088 PRELIMINARY; PRT; 282 AA.  
 AC Q9N088;  
 DT 01-OCT-2000 (TRENBLrel. 15, Created)  
 DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)  
 DT 01-OCT-2000 (TRENBLrel. 15, Last annotation update)  
 DE Unnamed protein product.  
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecoidea; Cercopithecinae; Macaca.  
 OX NCBI\_TaxID=9541;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21458551; PubMed=11574149; DOI=10.1016/S0378-1119(01)00665-5;  
 RA Osada N., Hida M., Kusuda J., Tanuma K., Iseki K., Hirata M., Suto Y.,  
 RA Hirai M., Terao K., Suzuki Y., Sugano S., Hashimoto K.;  
 RT "Assignment of 118 novel cDNAs of cynomolgus monkey brain to human  
 chromosomes.";  
 RL Gene 275:31-37(2001).  
 DR EMBL; AB046043; BAB01625.1; -.  
 SQ SEQUENCE 282 AA; 30104 MW; A3C249DD8E62F6D5 CRC64;  
 Query Match 49.5%; Score 54; DB 2; Length 282;  
 Best Local Similarity 62.5%; Pred. No. 36;  
 Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
 Qy 5 PPAHGVTSA PDTRPAP 20  
 Db 27 PPAQGSSSSPRTPPAP 42

Search completed: June 30, 2005, 06:50:02  
 Job time : 348 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 30, 2005, 05:38:37 ; Search time 67 Seconds  
(without alignments)  
28.721 Million cell updates/sec

Title: US-10-057-136-1

Perfect score: 109

Sequence: 1 GSTAPPAGVTSAPDTRPAP 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	109	100.0	1344	1 A35175	mucin 1 precursor,
2	104	95.4	347	2 S10571	mucin 1 precursor,
3	93	85.3	256	2 A60533	tumor-associated a
4	58.5	53.7	1334	2 T50568	probable multi-dom
5	52	47.7	244	2 A30722	conserved hypothet
6	52	47.7	739	1 A34873	transcription fact
7	52	47.7	739	2 I56187	transcription fact
8	52	47.7	766	1 A47001	transcription fact
9	52	47.7	770	1 S30293	transcription fact
10	51	46.8	241	2 AC2284	hypothetical prote
11	51	46.8	377	2 T36246	probable glycolate
12	51	46.8	594	2 T12995	pectinesterase hom
13	50.5	46.3	648	2 T35120	hypothetical prote
14	50	45.9	330	2 T05717	probable extensin
15	49.5	45.4	576	2 T36729	probable serine/th
16	49	45.0	30	2 T30514	hypothetical prote
17	49	45.0	428	2 T24769	hypothetical prote
18	49	45.0	630	2 A39344	tumor-associated m
19	49	45.0	631	2 I52257	episialin - mouse
20	48	44.0	250	2 S71348	Rieske iron-sulfur
21	48	44.0	322	2 E30457	Rieske iron-sulfur
22	48	44.0	324	2 C30440	Rieske iron-sulfur
23	48	44.0	551	2 F33015	hypothetical prote
24	48	44.0	691	2 A40024	regulatory protein
25	48	44.0	712	1 I46031	gelatinase B (EC 3
26	47	43.1	182	2 S73046	penicillin binding
27	47	43.1	411	2 D86995	probable D-alanyl-
28	47	43.1	526	2 T33047	hypothetical prote
29	47	43.1	544	2 A71260	hypothetical prote

RESULT 1

A35175

mucin 1 precursor, repetitive splice form A [validated] - human

N:Alternate names: breast carcinoma-associated DF3 antigen; core protein KP39; episialin

N:Contains: mucin 1 precursor, epithelial tumor antigen splice form; mucin 1 precursor,

C:Species: Homo sapiens (man)

C:Date: 20-Apr-2000 #sequence revision 20-Apr-2000 #text change 02-Jun-2000

C:Accession: A35175; B35175; A35886; A35887; S10572; S40293; A36735; PX0066; S10218; S51

R:Litgenberg, M.J.L.; Vos, H.L.; Gennissen, A.M.C.; Hilken, J.

J. Biol. Chem. 265, 5573-5578, 1990

A:Title: Episialin, a carcinoma-associated mucin, is generated by a polymorphic gene enc

A:Reference number: A35175; MUID:90202794; MUID:2318825

A:Accession: A35175

A:Molecule type: mRNA

A:Residues: 1-952,1033-1344 <LIC1>

A:Cross-references: GB:M32738; GB:J05288; NID:G182121; PIDN:AAA35804.1; PID:G182124; GB:

A:Experimental source: splice form A

A:Note: GenBank entries HUMEPIS1A1 and HUMEPIS1A2 present only the amino-and carboxyl-en

A:Accession: B35175

A:Molecule type: mRNA

A:Residues: 1-19,29-392,1033-1344 <LIC2>

A:Cross-references: GB:M32739; GB:J05288; NID:G182126; PIDN:AAA35806.1; PID:G182129; GB:

A:Experimental source: splice form B

A:Note: GenBank entries HUMEPIS1B1 and HUMEPIS1B2 present only the amino-and carboxyl-en

R:Gendler, S.J.; Lancaster, C.A.; Taylor-Papadimitriou, J.; Duhig, T.; Peat, N.; Burchel

J. Biol. Chem. 265, 15286-15293, 1990

A:Title: Molecular cloning and expression of human tumor-associated polymorphic epitheli

A:Reference number: A35886; MUID:90368715; PMID:1697589

A:Accession: A35886

A>Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-19,29-392,1033-1344 <GEN>

A:Cross-references: GB:J05581; NID:G188869; PIDN:AAA59876.1; PID:G188870

A:Note: GenBank entry HUMUCAB includes one copy of the tandemly repeated sequence

R:Lan, M.S.; Batra, S.K.; Qi, W.N.; Metzgar, R.S.; Hollingsworth, M.A.

J. Biol. Chem. 265, 15294-15299, 1990

A:Title: Cloning and sequencing of a human pancreatic tumor mucin cDNA.

A:Reference number: A35887; MUID:90368716; PMID:2394722

A:Accession: A35887

A>Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-19,29-1109,'S',1111-1339,'A',1341-1344 <LAN>

A:Cross-references: GB:J05582; NID:G189598; PIDN:AAA60019.1; PID:G189599

A:Note: GenBank entry HUMPANMU contains four fewer copies of the tandemly repeated sequ

R:Wreschner, D.H.; Hareuveni, M.; Tsarfay, I.; Smorodinsky, N.; Horev, J.; Zaretzky, J.

Eur. J. Biochem. 189, 463-473, 1990

A:Title: Human epithelial tumor antigen cDNA sequences. Differential splicing may genera

A:Reference number: S10571; MUID:90276413; PMID:2351132

A:Accession: S10572

A:Molecule type: mRNA

A:Residues: 1-19,29-155,'P',157-175,'P',177-182,'A',184-212,1033-1344 <WRE>

A;Cross-references: EMBL:X52229; NID:g37053  
R;Wreschner, D.H.  
Submitted to the EMBL Data Library, March 1990  
A;Reference number: S40293  
A;Accession: S40293  
A;Molecule type: mRNA  
A;Residues: 1-19,29-155,'P',157-175,'P',177-182,'A',184-212,1033-1037,'A',1039-1344 <WR2  
A;Cross-references: EMBL:X52229; NID:g37053; PIDN:CAA36478.1; PID:g37054  
R;Abe, M.; Siddiqui, J.; Kufe, D.  
Biochem. Biophys. Res. Commun. 165, 644-649, 1989  
A;Title: Sequence analysis of the 5' region of the human DF3 breast carcinoma-associated  
A;Reference number: A36735; MUID:90088473; PMID:2597151  
A;Accession: A36735  
A;Molecule type: mRNA  
A;Residues: 1-142,'Q',144-162,'Q',164-168 <ABE>  
A;Cross-references: EMBL:M31823; NID:g181542; PIDN:AAA35757.1; PID:g181543  
R;Masuzawa, Y.; Miyachi, T.; Hamaoui, M.; Ando, S.; Yoshida, J.; Takao, S.; Shimazu, H  
J. Biochem. 112, 609-615, 1992  
A;Title: A novel core protein as well as polymorphic epithelial mucin carry peanut agglu  
A;Reference number: JX0235; MUID:93123189; PMID:1478919  
A;Accession: EX0066  
A;Molecule type: mRNA  
A;Residues: 998-1011,'ES',1014-1017,1018-1032,'T',1034-1037,1038-1057 <MAS>  
A;Experimental source: Gastric carcinoma cell  
R;Zrihan-Licht, S.; Baruch, A.; Elroy-Stein, O.; Keydar, I.; Wreschner, D.H.  
FEBS Lett. 356, 130-136, 1994  
A;Title: Tyrosine phosphorylation of the MUC1 breast cancer membrane proteins cytokine  
A;Reference number: S51026; MUID:95080414; PMID:7988707  
A;Contents: annotation  
A;Note: undetermined tyrosine residues in the carboxyl-terminal non-repetitive region an  
C;Comment: This protein is length polymorphic. Individuals may have between 21 and 125 c  
partial repeats. The repeat shown is defined by SmaI nuclease sites.  
C;Comment: Serine and threonine residues in the tandem repeat domain are extensively gly  
C;Comment: For an alternative splice form without a tandem repeat domain, see PIR:S48146  
C;Genetics:  
A;Gene: GDB:MUC1; PUM  
A;Cross-references: GDB:120705; OMIM:158340  
A;Map position: 1q21-1q23  
A;Introns: 20/1; 62/3; 1165/3; 1184/2; 1230/1; 1270/3; 1320/3  
C;Superfamily: polymorphic epithelial mucin  
C;Keywords: alternative splicing; duplication; glycoprotein; phosphoprotein; polymorphis  
F;1-1344/Product: mucin 1 precursor, splice form A #status predicted <PREA>  
F;1-62/Region: mucin 1 amino-terminal non-repetitive  
F;1-23/Domain: signal sequence #link PREA #status predicted <SIGA>  
F;1-19,29-32/Domain: signal sequence #link PREB #status predicted <SIGB>  
F;1-19,29-1344/Product: mucin 1 precursor, splice form B #status predicted <PREB>  
F;1-19,29-212,1033-1344/Product: mucin 1 precursor, epithelial tumor antigen splice form  
F;138-1017/Region: 20-residue repeats (GSTAPPAHGVTSPDTRPAP)  
F;1143-1344/Region: mucin 1 carboxyl-terminal non-repetitive  
F;1245-1272/Domain: transmembrane #status predicted <TRM>  
F;1046,1064,1118,1144,1222/Binding site: carbohydrtate (Asn) (covalent) #status predicted  
F;1213/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 100.0%; Score 109; DB 1; Length 1344;  
Best Local Similarity 100.0%; Pred. No. 7.7e-07;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSTAPPAHGVTSPDTRPAP 20  
|||||  
Db 138 GSTAPPAHGVTSPDTRPAP 157  
|||||

RESULT 2  
S10571  
mucin 1 precursor, secreted epithelial tumor antigen splice form - human  
N;Contains: mucin 1 secreted breast-cancer-associated splice form  
C;Species: Homo sapiens (man)  
C;Date: 07-Apr-1994 #sequence revision 07-Apr-1994 #text\_change 09-Jul-2004  
C;Accession: S10571; JN0100; I56024; S09706; S10217  
R;Wreschner, D.H.; Hareuveni, M.; Tsarfaty, I.; Smorodinsky, N.; Horev, J.; Zaretsky, J.  
Eur. J. Biochem. 189, 463-473, 1990  
A;Title: Human epithelial tumor antigen cDNA sequences. Differential splicing may genera  
A;Reference number: S10571; MUID:90276413; PMID:2351132

A;Accession: S10571  
A;Molecule type: mRNA  
A;Residues: 1-347 <WRE>  
A;Cross-references: UNIPROT:Q9UMI8; EMBL:X52228; NID:g36434; PIDN:CAA36477.1; PID:g36435  
R;Tsarfaty, I.; Hareuveni, M.; Horev, J.; Zaretsky, J.; Weiss, M.; Jeltsch, J.M.; Garnie  
Gene 93, 313-318, 1990  
A;Title: Isolation and characterization of an expressed hypervariable gene coding for a l  
A;Reference number: JN0100; MUID:91033045; PMID:1688329  
A;Accession: JN0100  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-135,'Q',137-142,'E',144-163,204-208,'A',210-347 <TSA>  
A;Cross-references: GB:M35093; NID:g182252; PIDN:AAB59612.1; PID:g182253  
R;Xing, P.X.; Tjandra, J.J.; Reynolds, K.; McLaughlin, P.J.; Purcell, D.F.J.; McKenzie,  
J. Immunol. 142, 3503-3509, 1989  
A;Title: Reactivity of anti-human milk fat globule antibodies with synthetic peptides.  
A;Reference number: I56024; MUID:89235154; PMID:2715633  
A;Accession: I56024  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 182-201 <RES>  
A;Cross-references: GB:M26316; NID:g516622; PIDN:AAA36336.1; PID:g516623  
R;Tandler, S.J.B.  
Biochem. J. 267, 733-737, 1990  
A;Title: Elements of secondary structure in a human epithelial mucin core peptide fragmer  
A;Reference number: S09706; MUID:90253387; PMID:2339983  
A;Accession: S09706  
A;Molecule type: protein  
A;Residues: 182-201 <TEN>  
C;Genetics:  
A;Gene: GDB:MUC1; PUM  
A;Cross-references: GDB:120705; OMIM:158340  
A;Map position: 1q21-1q23  
C;Keywords: alternative splicing; tandem repeat  
F;1-23/Domain: signal sequence #status predicted <SIG>  
F;24-347/Product: mucin 1, secreted epithelial tumor antigen splice form #status predict  
F;24-163,204-347/Product: mucin 1, secreted breast-cancer-associated splice form #status

Query Match 95.4%; Score 104; DB 2; Length 347;  
Best Local Similarity 95.0%; Pred. No. 9.2e-07;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GSTAPPAHGVTSPDTRPAP 20  
|||||  
Db 129 GSTAPPAHGVTSPDTRPAP 148  
|||||

RESULT 3  
A60533  
tumor-associated antigen DF3 - human  
C;Species: Homo sapiens (man)  
C;Date: 19-Mar-1993 #sequence\_revision 07-May-1993 #text\_change 09-Jul-2004  
C;Accession: A60533  
R;Merlo, G.R.; Siddiqui, J.; Cropp, C.S.; Liscia, D.S.; Lidereau, R.; Callahan, R.; Kufe  
Cancer Res. 49, 6966-6971, 1989  
A;Title: Frequent alteration of the DF3 tumor-associated antigen gene in primary human b  
A;Reference number: A60533; MUID:90058554; PMID:2582438  
A;Accession: A60533  
A;Status: not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-256 <MER>  
A;Cross-references: UNIPROT:Q7M4M7  
C;Genetics:  
A;Map position: 1q21-q24  
C;Superfamily: proline-rich protein  
C;Keywords: glycoprotein; tandem repeat

Query Match 85.3%; Score 93; DB 2; Length 256;  
Best Local Similarity 85.0%; Pred. No. 2.1e-05;  
Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GSTAPPAHGVTSPDTRPAP 20  
|||||



Db 12 GSTAPPAHGVTSAPESRRAP 31

RESULT 4

T50568  
A;Molecule type: mRNA  
A;Residues: 1-77-96, 1996  
C;Species: Streptomyces coelicolor  
C;Superfamily: transcription factor Oct-1; homeobox homology; POU domain homology  
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation  
C;Date: 21-Jul-2000 #sequence\_revision 21-Jul-2000 #text\_change 09-Jul-2004  
C;Accession: T50568  
R;Redenbach, M.; Kleser, H.M.; Denaspate, D.; Eichner, A.; Cullum, J.; Kinashi, H.; Hopw Mol. Microbiol. 21, 77-96, 1996  
A;Title: A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb S  
A;Reference number: Z20556; MUID:97000351; PMID:8843436  
A;Accession: T50568  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-1334 <RED>  
A;Cross-references: UNIPROT:O9RKR9; EMBL:AL133220; PIDN:CAB61705.1  
A;Experimental source: strain A3(2)  
C;Genetics:  
A;Note: SCC75A.05c

Query Match 53.7%; Score 58.5; DB 2; Length 1334;

Best Local Similarity 68.4%; Pred. No. 5.2;

Matches 13; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

Qy 2 STAPPAHGVTSAPDTRRAP 20

||||| ||||| |||||

Db 328 STAPP-HDTASAADTAPAP 345

RESULT 5

AG0722  
conserved hypothetical protein STY1926 [imported] - Salmonella enterica subsp. enterica  
C;Species: Salmonella enterica subsp. enterica serovar Typhi  
A;Note: this species has also been called Salmonella typhi  
C;Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002  
C;Accession: AG0722  
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.  
Nature 413, 848-852, 2001  
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;  
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov  
A;Reference number: AB0502; MUID:21534947; PMID:11677608  
A;Accession: AG0722  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-244 <PAR>  
A;Cross-references: GB:AL513382; PIDN:CAD05481.1; PID:G16502985; GSPDB:GN00176  
C;Genetics:  
A;Gene: STY1926

Query Match 47.7%; Score 52; DB 2; Length 244;

Best Local Similarity 69.2%; Pred. No. 7.1;

Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 5 PPAHGVTSAPDTR 17

||||| ||||| |||||

Db 125 PPYGVTLTPDTR 137

RESULT 6

A34873  
transcription factor Oct-1, octamer-binding - chicken  
C;Species: Gallus gallus (chicken)  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C;Accession: A34873  
R;Petryniak, B.; Straudt, L.M.; Postema, C.E.; McCormack, W.T.; Thompson, C.B.  
Proc. Natl. Acad. Sci. U.S.A. 87, 1099-1103, 1990  
A;Title: Characterization of chicken octamer-binding proteins demonstrates that POU doma  
A;Reference number: A34873; MUID:90138945; PMID:1967834  
A;Accession: A34873

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-739 <PET>

A;Cross-references: UNIPROT:P15143; GB:M29972; NID:g212466; PIDN:AAA48993.1; PID:g212467

C;Superfamily: transcription factor Oct-1; homeobox homology; POU domain homology

C;Keywords: DNA binding; homeobox; nucleus; transcription regulation

F;281-348/Domain: POU domain homology <POU>

F;376-432/Domain: homeobox homology <HOX>

Query Match 47.7%; Score 52; DB 1; Length 739;

Best Local Similarity 47.4%; Pred. No. 22;

Matches 9; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 2 STAPPAHGVTSAPDTRRAP 20

||||| ||||| |||||

Db 506 STAPPASSAVTSPSLSPSP 524

RESULT 7

156187  
transcription factor Oct-1 - mouse (fragment)  
C;Species: Mus sp. (mouse)  
C;Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 20-Aug-1999  
C;Accession: I56187  
R;Lerner, A.; D'Adamo, L.; Diener, A.C.; Clayton, L.K.; Reinherz, E.L.  
J. Immunol. 151, 3152-3162, 1993  
A;Title: CD3 zeta/eta/theta locus is colinear with and transcribed antisense to the gene  
A;Reference number: I56187; MUID:93389142; PMID:8376772  
A;Accession: I56187  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-739 <RES>

A;Cross-references: GB:S65461; NID:g414379; PIDN:AA28234.1; PID:g414380

C;Superfamily: transcription factor Oct-1; homeobox homology; POU domain homology

C;Keywords: DNA binding; homeobox; nucleus; transcription regulation

F;281-348/Domain: POU domain homology <POU>

F;376-432/Domain: homeobox homology <HOX>

Query Match 47.7%; Score 52; DB 2; Length 739;

Best Local Similarity 47.4%; Pred. No. 22;

Matches 9; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 2 STAPPAHGVTSAPDTRRAP 20

||||| ||||| |||||

Db 507 STAPPASSAVTSPSLSPSP 525

RESULT 8

A47001  
transcription factor Oct-1 - human  
C;Species: Homo sapiens (man)  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 29-Sep-1999  
C;Accession: A47001; A31754  
R;Sturm, R.A.; Cassidy, J.L.; Das, G.; Romo, A.; Evans, G.A.  
Genomics 16, 333-341, 1993  
A;Title: Chromosomal structure and expression of the human OTF1 locus encoding the oct-1  
A;Reference number: A47001; MUID:93300505; PMID:8314572  
A;Accession: A47001

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-766 <STU>

A;Note: the sequence in GenBank entry HSOCT1, release 111.0, begins with Met-24

R;Sturm, R.A.; Das, G.; Herr, W.

Genes Dev. 2, 1582-1599, 1988

A;Title: The ubiquitous octamer-binding protein Oct-1 contains a POU domain with a homeo

A;Reference number: A31754; MUID:89107993; PMID:2905684

A;Accession: A31754

A;Molecule type: mRNA

A;Residues: 'P', 8-400, 'R', 402-766 <ST2>

A;Cross-references: GB:X13403; NID:g35126; PIDN:CAA31767.1; PID:g35127

C;Genetics:

A;Gene: GDB:POU2F1; OTF1; OCT1

A;Cross-references: GDB:120254; OMIM:164175

A:Map position: lq22-1q23  
C:Superfamily: transcription factor Oct-1, homeobox homology; POU domain homology  
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation  
F:310-377/Domain: POU domain homology <POU>  
F:403-459/Domain: homeobox homology <HOX>

Query Match 47.7%; Score 52; DB 1; Length 766;  
Best Local Similarity 47.4%; Pred. No. 22;  
Matches 9; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 2 STAPPAGHGVTSAPDTRPAP 20  
||||| :|||  
Db 533 STAPPASSAVTSPSLSPSP 551

RESULT 9  
S30293  
transcription factor Oct-1, splice form Oct-1A - mouse  
N:Alternate names: NP-A1; NF11; OBP100; OTF-1  
N:Contains: transcription factor Oct-1B  
C:Species: Mus musculus (house mouse)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004  
C:Accession: S30293; S30294; S31873; S31870; S09238; S53721; S53720; S22645; S26  
R:Suzuki, N.; Peter, W.; Ciesiolka, T.; Gruss, P.; Schoeler, H.R.  
Nucleic Acids Res. 21, 245-252, 1993  
A:Title: Mouse Oct-1 contains a composite homeodomain of human Oct-1 and Oct-2.  
A:Reference number: S30293; MUID:93181198; PMID:8441632  
A:Accession: S30293  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-770 <SUZ>  
A:Cross-references: UNIPROT:P25425; EMBL:X68362; NID:G53465; PIDN:CAA48422.1; PID:G53466  
A:Accession: S30294  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-498, 523-770 <SU2>  
A:Cross-references: EMBL:X68363; NID:G53471; PIDN:CAA48423.1; PID:G53472  
A:Accession: S30295  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-498, 523-716, 'DCFMDWRTF' <SU3>  
A:Cross-references: EMBL:X68364; NID:G53473; PIDN:CAA48424.1; PID:G53474  
A:Note: Splice form Oct-1C  
R:Jaffe, J.; Hochberg, M.; Reich, L.; Ben-neriah, Y.; Bergman, Y.; Laskov, R.  
submitted to the EMBL Data Library, February 1993  
A:Description: Expression of different isoforms of murine oct-1 gene in various tissues.  
A:Reference number: S31870  
A:Accession: S31873  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 30-128, 'P', 130-607, 'A', 609-667, 692-770 <JAF>  
A:Cross-references: EMBL:X70324; NID:G53467; PIDN:CAA49791.1; PID:G53468  
A:Accession: S31870  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 371-498, 523-607, 'A', 609-770 <JA2>  
A:Cross-references: EMBL:X70325  
R:Goldsbrough, A.; Ashworth, A.; Willison, K.  
Nucleic Acids Res. 18, 1634, 1990  
A:Title: Cloning and sequencing of POU-boxes expressed in mouse testis.  
A:Reference number: S09237; MUID:90221898; PMID:1970171  
A:Accession: S09238  
A:Molecule type: DNA  
A:Residues: 305-367, 'D', 369-426 <GOL>  
A:Cross-references: EMBL:X51958; NID:G53475; PIDN:CAA36217.1; PID:G930193  
R:Jaffe, J.; Hochberg, M.; Riss, J.; Hasin, T.; Reich, L.; Laskov, R.  
Biochim. Biophys. Acta 1261, 201-209, 1995  
A:Title: Cloning, sequencing and expression of two isoforms of the murine oct-1 transcri  
A:Reference number: S53720; MUID:95226446; PMID:7711063  
A:Accession: S53721  
A:Status: preliminary; nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 30-128, 'P', 130-607, 'A', 609-667, 692-770 <JA3>

A:Cross-references: EMBL:X70324; NID:G53467; PIDN:CAA49791.1; PID:G53468  
A:Accession: S53720  
A:Status: preliminary; nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 370-498, 523-607, 'A', 609-770 <JA4>  
A:Cross-references: EMBL:X70325; NID:G53469; PIDN:CAA49792.1; PID:G53470  
R:Stepchenko, A.G.  
Nucleic Acids Res. 20, 1419, 1992  
A:Title: The nucleotide sequence of mouse OCT-1 cDNA.  
A:Reference number: S22645; MUID:92220620; PMID:1561098  
A:Accession: S22645  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 'MLDCSDCVLDSR', 1-42, 'L', 44-53, 72-498, 523-607, 'A', 609-638 <STE>  
A:Cross-references: EMBL:X56230; NID:G53476; PIDN:CAA39679.1; PID:G53477  
C:Genetics:  
A:Gene: Oct-1  
A:Map position: 1  
C:Superfamily: transcription factor Oct-1; homeobox homology; POU domain homology  
C:Keywords: alternative splicing; DNA binding; homeobox; nucleus; transcription regulati  
F:1-770/Product: transcription factor Oct-1A #status predicted <OC1A>  
F:1-498, 523-770/Product: transcription factor Oct-1B #status predicted <OC1B>  
F:288-355/Domain: POU domain homology <POU>  
F:383-439/Domain: homeobox homology <HOX>

Query Match 47.7%; Score 52; DB 1; Length 770;  
Best Local Similarity 47.4%; Pred. No. 23;  
Matches 9; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 2 STAPPAGHGVTSAPDTRPAP 20  
||||| :|||  
Db 538 STAPPASSAVTSPSLSPSP 556

RESULT 10  
AC2284  
hypothetical protein all13826 [imported] - Nostoc sp. (strain PCC 7120)  
C:Species: Nostoc sp. PCC 7120  
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C:Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004  
A:Accession: AC2284  
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi  
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.  
DNA Res. 8, 205-213, 2001  
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana  
A:Reference number: AB1807; MUID:21595285; PMID:11759840  
A:Accession: AC2284  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-241 <KUR>  
A:Cross-references: UNIPROT:Q8YQJ7; GB:BA000019; PIDN:BAF75525.1; PID:gl7132960; GSPDB:G  
A:Experimental source: strain PCC 7120  
C:Genetics:  
A:Gene: all13826

Query Match 46.8%; Score 51; DB 2; Length 241;  
Best Local Similarity 61.1%; Pred. No. 9.5;  
Matches 11; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 3 TAPPAGHGVTSAPDTRPAP 20  
||||| :|||  
Db 182 TAKPAASTSKPTTSPAP 199

RESULT 11  
T36246  
probable glycolate oxidase - Streptomyces coelicolor  
C:Species: Streptomyces coelicolor  
C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
A:Accession: T36246  
R:Saunders, D.C.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.  
submitted to the EMBL Data Library, March 1999  
A:Reference number: Z21602

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A:Accession: T36246
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-377 <SAU>
A:Cross-references: UNIPROT:Q924X8; EMBL:AL035640; PIDN:CAB38520.1; GSPDB:GN00070; SCOE
C:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCOE:SC63.05
C:Superfamily: alpha-hydroxy acid dehydrogenase, FMN-dependent; (S)-2-hydroxy-acid oxida
F:2-296/Domain: (S)-2-hydroxy-acid oxidase homology <2HY>

Query Match 46.8%; Score 51; DB 2; Length 377;
Best Local Similarity 64.7%; Pred. No. 15;
Matches 11; Conservative 1; Mismatches 3; Indels 2; Gaps 1;

QY 4 APPAHGVTSAPTTRPAP 20
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DB 356 APPHGPPTAP--RDAP 370

RESULT 12
T12995
pectinesterase homolog T21L8.150 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C:Accession: T12995
R:Choisne, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artiguenave, F.; Sa
submitted to the Protein Sequence Database, July 1999
A:Reference number: Z17586
A:Accession: T12995
A:Molecule type: DNA
A:Residues: 1-594 <CHO>
A:Cross-references: UNIPROT:Q9SVY3; EMBL:AL096860; GSPDB:GN00061; ATSP:T21L8.150
A:Experimental source: cultivar Columbia; BAC clone T21L8
C:Genetics:
A:Gene: ATSP:T21L8.150
A:Map position: 3
A:Introns: 251/1; 363/1
C:Superfamily: pectinesterase

Query Match 46.8%; Score 51; DB 2; Length 594;
Best Local Similarity 45.5%; Pred. No. 24;
Matches 10; Conservative 4; Mismatches 6; Indels 2; Gaps 1;

QY 1 GSTAPPA--HGVTSAFPTTRPAP 20
|||:|:|:|:|
DB 31 GTDAPPWHDHNVSPPTAPSP 52

RESULT 13
T35120
hypothetical protein SC4H2.21 SC4H2.21 - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C:Accession: T35120
R:Seeger, K.J.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, March 1998
A:Reference number: Z21568
A:Accession: T35120
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-648 <SEE>
A:Cross-references: UNIPROT:Q69976; EMBL:AL022268; PIDN:CAA18348.1; GSPDB:GN00070; SCOE
C:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCOE:SC4H2.21
C:Superfamily: Escherichia coli plasmid ColV-K30 aerobactin biosynthesis protein iuca

Query Match 46.3%; Score 50.5; DB 2; Length 648;
Best Local Similarity 61.9%; Pred. No. 30;
Matches 13; Conservative 0; Mismatches 3; Indels 5; Gaps 2;

QY 3 TAP---PAHGVTSAFPTTRPAP 20
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Db 52 TAPRLAPAHGVLPGP--RPAP 70
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RESULT 14
T05717
probable extensin - barley (fragment)
C:Species: Hordeum vulgare (barley)
C:Date: 09-Apr-1999 #sequence_revision 09-Apr-1999 #text_change 09-Jul-2004
C:Accession: T05717
R:Doan, D.N.P.; Sturaro, M.; Olsen, O.A.
submitted to the EMBL Data Library, July 1997
A:Description: Characterization of a nuclear cDNA encoding a probable extensin from dev
A:Reference number: Z15429
A:Accession: T05717
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-330 <DOA>
A:Cross-references: UNIPROT:O49870; EMBL:Z98204; PIDN:CAB10894.1
C:Genetics:
A:Gene: exl
A:Map position: 2
C:Superfamily: hydroxyproline-rich glycoprotein

Query Match 45.9%; Score 50; DB 2; Length 330;
Best Local Similarity 50.0%; Pred. No. 18;
Matches 10; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 GSTAPPAHGVTSAFPTTRPAP 20
|||||:|:|:|
DB 47 GSQAPPTYSPPTAKPTTPAP 66

RESULT 15
T36729
probable serine/threonine-specific protein kinase (EC 2.7.1.1) - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 16-Aug-2004
C:Accession: T36729
R:Murphy, L.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, June 1999
A:Reference number: Z21612
A:Accession: T36729
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-576 <MUR>
A:Cross-references: UNIPROT:Q9XA04; EMBL:AL079308; PIDN:CAB45227.1; GSPDB:GN00070; SCOE
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCOE:DB:SCH69.30
C:Superfamily: protein kinase homology
C:Keywords: phosphotransferase; serine/threonine-specific protein kinase

Query Match 45.4%; Score 49.5; DB 2; Length 576;
Best Local Similarity 56.0%; Pred. No. 37;
Matches 14; Conservative 0; Mismatches 6; Indels 5; Gaps 2;

QY 1 GSTAPP-AHGVTSAFPTTRPAP 20
|||||:|:|:|
DB 399 GFTAPPSAPSAPSAPSAGPTTRPAP 423

Search completed: June 30, 2005, 06:44:09
Job time : 68 secs
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GenCore version 5.1.6  
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# OM protein - protein search, using sw model

Run on: June 30, 2005, 06:29:25 ; Search time 1315 Seconds  
(without alignments)  
1.135 Million cell updates/sec

Title: US-10-057-136-1

Perfect score: 109

Sequence: 1 GSTAPPAHGVTSPDTRPAP 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.\*

- 1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*
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- 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*
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- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	109	100.0	20	4	US-09-641-833-1
2	109	100.0	30	3	US-08-737-896-6
3	109	100.0	30	4	US-09-593-870A-47
4	109	100.0	30	5	PCT-US96-09951-6
5	109	100.0	32	4	US-09-593-870A-46
6	109	100.0	40	1	US-08-099-354-1
7	109	100.0	40	2	US-08-288-059-7
8	103	94.5	25	4	US-09-497-232-5
9	99	90.8	24	3	US-08-737-896-5
10	99	90.8	24	4	US-09-497-232-23
11	99	90.8	24	5	PCT-US96-09951-5
12	99	90.8	25	4	US-09-217-306B-3
13	98	89.9	30	3	US-08-134-198E-13
14	95	87.2	177	4	US-09-646-028-54
15	94	86.2	20	3	US-08-134-198E-35
16	92	84.4	24	4	US-09-217-306B-16
17	92	84.4	24	4	US-09-217-306B-17
18	91	83.5	28	2	US-08-488-161-9
19	91	83.5	28	3	PCT-US95-11934-9
20	91	83.5	28	5	PCT-US95-11934-9
21	91	83.5	1867	3	US-08-479-537A-5
22	91	83.5	1867	3	US-09-083-116-5
23	91	83.5	1867	3	US-09-134-916A-5
24	91	83.5	2035	2	US-08-479-537A-2
25	91	83.5	2035	3	US-09-083-116-2
26	91	83.5	2035	3	US-09-134-916A-2
27	90	82.6	172	4	US-09-646-028-49

28	87	79.8	40	1	US-08-099-354-2	Sequence 2, Appli
29	87	79.8	40	2	US-08-288-059-8	Sequence 8, Appli
30	84	77.1	20	2	US-08-479-537A-3	Sequence 3, Appli
31	84	77.1	20	3	US-09-083-116-3	Sequence 3, Appli
32	84	77.1	20	3	US-09-134-916A-3	Sequence 8, Appli
33	83	76.1	20	3	US-08-833-807-8	Sequence 8, Appli
34	83	76.1	20	3	US-09-223-043-8	Sequence 1, Appli
35	83	76.1	20	3	US-09-291-351-1	Sequence 16, Appli
36	83	76.1	20	3	US-08-043-731-16	Sequence 20, Appli
37	83	76.1	20	4	US-09-593-870A-20	Sequence 7, Appli
38	83	76.1	21	2	US-08-833-807-7	Sequence 7, Appli
39	83	76.1	21	3	US-09-223-043-7	Sequence 15, Appli
40	83	76.1	21	3	US-09-043-731-15	Sequence 19, Appli
41	83	76.1	21	4	US-09-593-870A-19	Sequence 17, Appli
42	81	74.3	23	3	US-09-043-731-17	Sequence 2, Appli
43	77	70.6	134	4	US-09-646-028-1	Sequence 1, Appli
44	77	70.6	137	4	US-09-646-028-2	Sequence 2, Appli
45	77	70.6	138	4	US-09-646-028-3	Sequence 3, Appli

## ALIGNMENTS

### RESULT 1

US-09-641-833-1  
; Sequence 1, Application US/09641833  
; Patent No. 6716966  
; GENERAL INFORMATION:  
; APPLICANT: Madiyalakan, Ragupathy  
; TITLE OF INVENTION: Therapeutic Binding Agents Against MUC-1 Antigen and  
; TITLE OF INVENTION: Methods  
; TITLE OF INVENTION: for Their Use  
; FILE REFERENCE: 107823.127  
; CURRENT APPLICATION NUMBER: US/09/641.833  
; CURRENT FILING DATE: 2000-08-16  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: MUC-1 antigen  
US-09-641-833-1

Query Match 100.0%; Score 109; DB 4; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2e-08;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSTAPPAHGVTSPDTRPAP 20  
| | | | | | | | | | | | | | | | | | | | | |  
Db 1 GSTAPPAHGVTSPDTRPAP 20

### RESULT 2

US-08-737-896-6  
; Sequence 6, Application US/08737896  
; Patent No. 6168804  
; GENERAL INFORMATION:  
; APPLICANT: Samuel, John  
; APPLICANT: Kwon, Glen S.  
; TITLE OF INVENTION: METHOD FOR ELICITING TH1-SPECIFIC  
; TITLE OF INVENTION: IMMUNE RESPONSE  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 4225 Executive Square, Suite 1400  
; CITY: La Jolla  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette

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; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/737,896
; FILING DATE: 24-SEP-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/480,499
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: PCT/US96/09551
; FILING DATE: 07-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07254/037001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; CLONE: SPI-070 MUC1
; US-08-737-896-6

Query Match 100.0%; Score 109; DB 3; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.1e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSTAPPAHGVTSA PDTRAP 20
Db 5 GSTAPPAHGVTSA PDTRAP 24

RESULT 3
US-09-593-870A-47
; Sequence 47, Application US/09593870A
; Patent No. 6548643
; GENERAL INFORMATION:
; APPLICANT: McKenzie, Ian F.C.
; APPLICANT: Apostolopoulos, Vasso
; APPLICANT: Pietersz, Geoff Allan
; TITLE OF INVENTION: Antigen Carbohydrate Compounds and Their
; FILE REFERENCE: 2368-McKenzie
; CURRENT APPLICATION NUMBER: US/09/593,870A
; CURRENT FILING DATE: 2000-06-14
; PRIOR FILING DATE: 1998-12-30
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 47
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-593-870A-47

Query Match 100.0%; Score 109; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.1e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSTAPPAHGVTSA PDTRAP 20
Db 8 GSTAPPAHGVTSA PDTRAP 27

RESULT 4
PCT-US96-09951-6
; Sequence 6, Application PC/TUS9609951
; GENERAL INFORMATION:
; APPLICANT: The Governors of the University of Alberta
; TITLE OF INVENTION: A METHOD FOR ELICITING A THI-SPECIFIC
; IMMUNE RESPONSE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: California
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/09951
; FILING DATE: 06-JUN-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Learn, June M.
; REGISTRATION NUMBER: 31,238
; REFERENCE/DOCKET NUMBER: 07254/037W01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 678-5070
; TELEFAX: (619) 678-5099
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; CLONE: SPI-070 MUC1
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..30
; PCT-US96-09951-6

Query Match 100.0%; Score 109; DB 5; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.1e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSTAPPAHGVTSA PDTRAP 20
Db 5 GSTAPPAHGVTSA PDTRAP 24

RESULT 5
US-09-593-870A-46
; Sequence 46, Application US/09593870A
; Patent No. 6548643
; GENERAL INFORMATION:
; APPLICANT: McKenzie, Ian F.C.
; APPLICANT: Apostolopoulos, Vasso
; APPLICANT: Pietersz, Geoff Allan
; TITLE OF INVENTION: Antigen Carbohydrate Compounds and Their
; FILE REFERENCE: 2368-McKenzie
; CURRENT APPLICATION NUMBER: US/09/593,870A
; CURRENT FILING DATE: 2000-06-14
; PRIOR FILING DATE: 1998-12-30
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 46
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-593-870A-46
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Query Match 100.0%; Score 109; DB 4; Length 32;  
Best Local Similarity 100.0%; Pred. No. 3.4e-08;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSTAPPAHGVTSPDTRPAP 20  
| | | | | | | | | | | | | | | | | | | | | |  
Db 8 GSTAPPAHGVTSPDTRPAP 27

RESULT 6  
US-08-099-354-1  
; Sequence 1, Application US/08099354  
; Patent No. 5744144  
; GENERAL INFORMATION:  
; APPLICANT: FINN, OLIVERA J.  
; APPLICANT: FONTENOT, J. D.  
; APPLICANT: MONTELLARO, RONALD C.  
; TITLE OF INVENTION: SYNTHETIC MULTIPLE TANDEM REPEAT MUCIN  
; TITLE OF INVENTION: AND MUCIN-LIKE PEPTIDES, AND USES THEREOF  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN  
; STREET: 1100 NEW YORK AVENUE, N.W.  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/099,354  
; FILING DATE: 30-JUL-1993  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SIRILLA, GEORGE M.  
; REGISTRATION NUMBER: 18221  
; REFERENCE/DOCKET NUMBER: 6137/202246  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-861-3536  
; TELEFAX: 202-822-0944  
; TELEX: 6714627 CUSH  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 40 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-099-354-1

Query Match 100.0%; Score 109; DB 1; Length 40;  
Best Local Similarity 100.0%; Pred. No. 4.3e-08;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSTAPPAHGVTSPDTRPAP 20  
| | | | | | | | | | | | | | | | | | | | | |  
Db 9 GSTAPPAHGVTSPDTRPAP 28

RESULT 7  
US-08-288-059-7  
; Sequence 7, Application US/08288059  
; Patent No. 5827666  
; GENERAL INFORMATION:  
; APPLICANT: FINN, OLIVERA J.  
; APPLICANT: FONTENOT, J. D.  
; APPLICANT: MONTELLARO, RONALD C.  
; TITLE OF INVENTION: SYNTHETIC MULTIPLE TANDEM REPEAT MUCIN  
; TITLE OF INVENTION: AND MUCIN-LIKE PEPTIDES, AND USES THEREOF  
; NUMBER OF SEQUENCES: 36

; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN, L.L.P.  
; STREET: 1100 NEW YORK AVENUE, N.W.  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/288,059  
; FILING DATE: 08-AUG-1994  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CHAPIN, MARLANA K.  
; REGISTRATION NUMBER: 35,843  
; REFERENCE/DOCKET NUMBER: 61137/205204  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-861-3711  
; TELEFAX: 202-822-0944  
; TELEX: 6714627 CUSH  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 40 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-288-059-7

Query Match 100.0%; Score 109; DB 2; Length 40;  
Best Local Similarity 100.0%; Pred. No. 4.3e-08;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSTAPPAHGVTSPDTRPAP 20  
| | | | | | | | | | | | | | | | | | | | | |  
Db 9 GSTAPPAHGVTSPDTRPAP 28

RESULT 8  
US-09-497-232-5  
; Sequence 5, Application US/09497232  
; Patent No. 6600012  
; GENERAL INFORMATION:  
; APPLICANT: AGRAWAL, Babita  
; APPLICANT: KRANTZ, Mark J.  
; REDDISH, Mark A.  
; LONGENECKER, B. Michael  
; TITLE OF INVENTION: METHOD FOR GENERATING ACTIVATED T-CELLS  
; AND ANTIGEN-PULSED ANTIGEN-PRESENTING CELLS  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FOLEY & LARDNER  
; STREET: 3000 K Street, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/497,232  
; FILING DATE: 03-Feb-2000  
; CLASSIFICATION: <unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/074,410  
; FILING DATE: 08-MAY-1998

APPLICATION NUMBER: US 60/045,949  
FILING DATE: 08-MAY-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Saxe, Bernhard D.  
REGISTRATION NUMBER: 28,665  
REFERENCE/DOCKET NUMBER: 042881/0114  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 25 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-09-497-232-5

Query Match 94.5%; Score 103; DB 4; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.6e-07;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 STAPPAHGVTSPDTRPAP 20  
| | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 1 STAPPAHGVTSPDTRPAP 19

RESULT 9  
US-08-737-896-5  
Sequence 5, Application US/08737896  
Patent No. 6168804  
GENERAL INFORMATION:  
APPLICANT: Samuel, John  
TITLE OF INVENTION: METHOD FOR ELICITING TH1-SPECIFIC  
IMMUNE RESPONSE  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 4225 Executive Square, Suite 1400  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/737,896  
FILING DATE: 24-SEP-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/480,499  
FILING DATE: 07-JUN-1996  
APPLICATION NUMBER: PCT/US96/09551  
FILING DATE: 07-JUN-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Haile, Lisa A.  
REGISTRATION NUMBER: 38,347  
REFERENCE/DOCKET NUMBER: 07254/037001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619/678-5070  
TELEFAX: 619/678-5099  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
CLONE: SPQ-065 MUC1

US-08-737-896-5

Query Match 90.8%; Score 99; DB 3; Length 24;  
Best Local Similarity 100.0%; Pred. No. 5.4e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TAPPAHGVTSPDTRPAP 20  
| | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 1 TAPPAHGVTSPDTRPAP 18

RESULT 10  
US-09-497-232-23  
Sequence 23, Application US/09497232  
Patent No. 6600012  
GENERAL INFORMATION:  
APPLICANT: AGRAWAL, Babita  
KRANTZ, Mark J.  
REDDISH, Mark A.  
LONGENECKER, B. Michael  
TITLE OF INVENTION: METHOD FOR GENERATING ACTIVATED T-CELLS  
AND ANTIGEN-PULSED ANTIGEN-PRESENTING CELLS  
NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FOLEY & LARDNER  
STREET: 3000 K Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/497,232  
FILING DATE: 03-Feb-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/074,410  
FILING DATE: 08-MAY-1998  
APPLICATION NUMBER: US 60/045,949  
FILING DATE: 08-MAY-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Saxe, Bernhard D.  
REGISTRATION NUMBER: 28,665  
REFERENCE/DOCKET NUMBER: 042881/0114  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 23:  
US-09-497-232-23

Query Match 90.8%; Score 99; DB 4; Length 24;  
Best Local Similarity 100.0%; Pred. No. 5.4e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TAPPAHGVTSPDTRPAP 20  
| | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 1 TAPPAHGVTSPDTRPAP 18

RESULT 11  
PCT-US96-09951-5  
Sequence 5, Application PC/TUS9609951



GENERAL INFORMATION:  
APPLICANT: The Governors of the University of Alberta  
TITLE OF INVENTION: A METHOD FOR ELICITING A THI-SPECIFIC  
TITLE OF INVENTION: IMMUNE RESPONSE  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 4225 Executive Square, Suite 1400  
CITY: La Jolla  
STATE: California  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/09951  
FILING DATE: 06-JUN-1996  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Learn, June M.  
REGISTRATION NUMBER: 31,238  
REFERENCE/DOCKET NUMBER: 07254/037W01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 678-5070  
TELEFAX: (619) 678-5099  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
CLONE: SPQ-065 MUC1  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..24  
PCT-US96-09951-5

Query Match 90.8%; Score 99; DB 5; Length 24;  
Best Local Similarity 100.0%; Pred. No. 5.4e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TAPPAHGVTSPDTRPAP 20  
Db 1 TAPPAHGVTSPDTRPAP 18

RESULT 12  
US-09-217-306B-3  
Sequence 3, Application US/09217306B  
Patent No. 6465220  
GENERAL INFORMATION:  
APPLICANT: Hassen, Helle  
APPLICANT: Clausen, Henrik  
APPLICANT: Bennett, Eric P.  
TITLE OF INVENTION: Glycosylation Using Galnac-T4 Transferase  
FILE REFERENCE: 8850\*1  
CURRENT APPLICATION NUMBER: US/09/217.306B  
CURRENT FILING DATE: 1998-12-21  
NUMBER OF SEQ ID NOS: 25  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 3  
LENGTH: 25  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: REPEAT  
LOCATION: (1)..(25)  
OTHER INFORMATION: MUC-1 tandem repeat

US-09-217-306B-3

Query Match 90.8%; Score 99; DB 4; Length 25;  
Best Local Similarity 100.0%; Pred. No. 5.7e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TAPPAHGVTSPDTRPAP 20  
Db 1 TAPPAHGVTSPDTRPAP 18

RESULT 13  
US-08-134-198E-13  
Sequence 13, Application US/08134198E  
Patent No. 6190885  
GENERAL INFORMATION:  
APPLICANT: CANCER RESEARCH FUND  
APPLICANT: OF CONTRA COSTA  
APPLICANT: PETERSON, JERRY A.  
APPLICANT: LARocca, DAVID J.  
TITLE OF INVENTION: FUSION PROTEIN CONTAINING HMEG  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pretty, Schroeder & Poplawski  
STREET: 444 South Flower Street, Suite 1900  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0,  
SOFTWARE: Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/134,198E  
FILING DATE: October 8, 1993  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Amzel, Viviana  
REGISTRATION NUMBER: 30,930  
REFERENCE/DOCKET NUMBER: P66 38208 (CRFC-003C)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 622-7700  
TELEFAX: (213) 489-4210  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 30  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-134-198E-13

Query Match 89.9%; Score 98; DB 3; Length 30;  
Best Local Similarity 100.0%; Pred. No. 9.4e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSTAPPAHGVTSPDTRP 18  
Db 13 GSTAPPAHGVTSPDTRP 30

RESULT 14  
US-09-646-028-54  
Sequence 54, Application US/09646028  
Patent No. 6562347  
GENERAL INFORMATION:  
APPLICANT: Kwak, Larry  
APPLICANT: Biragyn, Arya  
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF  
TITLE OF INVENTION: CHEMOKINE-TUMOR ANTIGEN FUSION PROTEINS AS CANCER VACCINES



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 30, 2005, 06:39:50 ; Search time 349 Seconds  
(without alignments)  
22.109 Million cell updates/sec

Title: US-10-057-136-1

Perfect score: 109

Sequence: 1 GSTAPPAGHGVTSAPDTRPAP 20

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 1722976 seqs, 385795295 residues

Total number of hits satisfying chosen parameters: 1722976

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*
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- 9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep.\*
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- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
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- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US10E\_PUBCOMB.pep.\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/2/pubpaa/US11A\_PUBCOMB.pep.\*
- 20: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*
- 21: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 22: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	ID	Description
1	109	100.0	20 9 US-09-994-466-1	Sequence 1, Appli
2	109	100.0	20 14 US-10-057-136-1	Sequence 1, Appli
3	109	100.0	20 17 US-10-754-089-1	Sequence 1, Appli
4	109	100.0	31 9 US-09-994-466-11	Sequence 11, Appli
5	109	100.0	40 10 US-09-996-069-9	Sequence 9, Appli
6	109	100.0	40 17 US-10-635-211-4	Sequence 4, Appli
7	109	100.0	43 14 US-10-106-876-14	Sequence 14, Appli
8	109	100.0	46 10 US-09-996-069-5	Sequence 5, Appli
9	109	100.0	46 14 US-10-106-876-1	Sequence 1, Appli
10	109	100.0	100 9 US-09-965-131-6	Sequence 6, Appli
11	109	100.0	159 17 US-10-635-211-9	Sequence 9, Appli

12	109	100.0	475	15	US-10-417-312-1	Sequence 1, Appli
13	109	100.0	475	17	US-10-696-639-59	Sequence 59, Appli
14	109	100.0	508	14	US-10-057-136-20	Sequence 20, Appli
15	109	100.0	586	17	US-10-635-211-2	Sequence 2, Appli
16	109	100.0	1255	10	US-09-996-069-10	Sequence 10, Appli
17	109	100.0	1255	14	US-10-171-311-158	Sequence 158, App
18	109	100.0	1255	14	US-10-177-293-311	Sequence 311, App
19	109	100.0	1255	16	US-10-734-564-120	Sequence 120, App
20	109	100.0	1255	17	US-10-473-484-2	Sequence 2, Appli
21	104	95.4	515	14	US-10-097-340-212	Sequence 212, App
22	104	95.4	515	14	US-10-171-311-156	Sequence 156, App
23	104	95.4	515	15	US-10-612-090-19	Sequence 19, Appli
24	103	94.5	26	9	US-09-815-346-5	Sequence 5, Appli
25	103	94.5	26	14	US-10-106-876-8	Sequence 8, Appli
26	103	94.5	27	9	US-09-870-631-1	Sequence 1, Appli
27	103	94.5	27	9	US-09-999-191-1	Sequence 1, Appli
28	103	94.5	27	14	US-10-106-876-12	Sequence 12, Appli
29	103	94.5	28	14	US-10-106-876-13	Sequence 13, Appli
30	100	91.7	20	14	US-10-057-136-16	Sequence 16, Appli
31	99	90.8	20	9	US-09-984-333-9	Sequence 9, Appli
32	99	90.8	24	14	US-10-292-896-2	Sequence 2, Appli
33	99	90.8	24	17	US-10-705-401-2	Sequence 2, Appli
34	99	90.8	25	10	US-09-881-339-3	Sequence 3, Appli
35	99	90.8	25	15	US-10-417-633-3	Sequence 3, Appli
36	99	90.8	27	9	US-09-815-346-4	Sequence 4, Appli
37	99	90.8	27	14	US-10-106-876-7	Sequence 7, Appli
38	99	90.8	27	14	US-10-106-876-9	Sequence 9, Appli
39	98.5	90.4	35	16	US-10-471-607-15	Sequence 15, Appli
40	98.5	90.4	49	16	US-10-471-607-14	Sequence 14, Appli
41	98.5	90.4	49	16	US-10-471-607-16	Sequence 16, Appli
42	97	89.0	20	14	US-10-057-136-17	Sequence 17, Appli
43	95	87.2	26	14	US-10-106-876-20	Sequence 20, Appli
44	95	87.2	177	14	US-10-335-394-54	Sequence 54, Appli
45	94	86.2	25	14	US-10-292-896-9	Sequence 9, Appli

#### ALIGNMENTS

RESULT 1  
US-09-994-466-1  
; Sequence 1, Application US/09994466  
; Publication No. US20020132771A1  
; GENERAL INFORMATION:  
; APPLICANT: Madiyalakan, R.  
; TITLE OF INVENTION: THERAPEUTIC BINDING AGENTS AGAINST MUC-1 ANTIGEN AND METHODS FOR  
; FILE REFERENCE: THEIR USE  
; FILE REFERENCE: AREX-P03-002  
; CURRENT APPLICATION NUMBER: US/09/994,466  
; CURRENT FILING DATE: 2001-11-26  
; PRIOR APPLICATION NUMBER: 09/724094  
; PRIOR FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-994-466-1

Query Match 100.0%; Score 109; DB 9; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.3e-07;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSTAPPAGHGVTSAPDTRAP 20  
DB 1 GSTAPPAGHGVTSAPDTRAP 20

RESULT 2  
US-10-057-136-1  
; Sequence 1, Application US/10057136  
; Publication No. US20030021770A1

```
; GENERAL INFORMATION:
; APPLICANT: SCHLOM, JEFFREY
; APPLICANT: KANTOR, JUDITH
; APPLICANT: KUFE, DONALD
; APPLICANT: PANICALI, DENNIS
; APPLICANT: GRITZ, LINDA
; TITLE OF INVENTION: RECOMBINANT POX VIRUS FOR IMMUNIZATION AGAINST MUC1
; TITLE OF INVENTION: TUMOR-ASSOCIATED ANTIGEN
; FILE REFERENCE: 700953/47113C
; CURRENT APPLICATION NUMBER: US/10/057,136
; CURRENT FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: 09/366,670
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: PCT/US98/03693
; PRIOR FILING DATE: 1998-02-24
; PRIOR APPLICATION NUMBER: 60/038,253
; PRIOR FILING DATE: 1997-02-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-057-136-1

Query Match      100.0%; Score 109; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e-07;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GSTAPPAHGVTSA PDTRPAP 20
Db      1 GSTAPPAHGVTSA PDTRPAP 20
|||||

RESULT 3
US-10-754-089-1
; Sequence 1, Application US/10754089
; Publication No. US20050048059A1
; GENERAL INFORMATION:
; APPLICANT: Madiyalakan, Ragupathy
; TITLE OF INVENTION: Therapeutic Binding Agents Against MUC-1 Antigen and
; TITLE OF INVENTION: Methods
; TITLE OF INVENTION: for Their Use
; FILE REFERENCE: 107823.127
; CURRENT APPLICATION NUMBER: US/10/754,089
; CURRENT FILING DATE: 2004-01-07
; PRIOR APPLICATION NUMBER: US/09/641,833
; PRIOR FILING DATE: 2000-08-18
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MUC-1 antigen
US-10-754-089-1

Query Match      100.0%; Score 109; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e-07;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GSTAPPAHGVTSA PDTRPAP 20
Db      1 GSTAPPAHGVTSA PDTRPAP 20
|||||

RESULT 4
US-09-994-466-11
; Sequence 11, Application US/09994466
; Publication No. US20020132771A1
; GENERAL INFORMATION:
; APPLICANT: Madiyalakan, R.
```

```
; TITLE OF INVENTION: THERAPEUTIC BINDING AGENTS AGAINST MUC-1 ANTIGEN AND METHODS FOR
; TITLE OF INVENTION: THEIR USE
; FILE REFERENCE: AREX-P03-002
; CURRENT APPLICATION NUMBER: US/09/994,466
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 09/724094
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-994-466-11

Query Match      100.0%; Score 109; DB 9; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GSTAPPAHGVTSA PDTRPAP 20
Db      9 GSTAPPAHGVTSA PDTRPAP 28
|||||

RESULT 5
US-09-996-069-9
; Sequence 9, Application US/09996069
; Publication No. US20030036199A1
; GENERAL INFORMATION:
; APPLICANT: Bamdad, Cynthia
; APPLICANT: Bamdad, R. Shoshana
; TITLE OF INVENTION: DIAGNOSTIC TUMOR MARKERS, DRUG SCREENING FOR TUMORIGENESIS INHIBI
; TITLE OF INVENTION: AND COMPOSITIONS AND METHODS FOR TREATMENT OF CANCER
; FILE REFERENCE: M01015/70071
; CURRENT APPLICATION NUMBER: US/09/996,069
; CURRENT FILING DATE: 2001-11-27
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-069-9

Query Match      100.0%; Score 109; DB 10; Length 40;
Best Local Similarity 100.0%; Pred. No. 4.6e-07;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GSTAPPAHGVTSA PDTRPAP 20
Db      8 GSTAPPAHGVTSA PDTRPAP 27
|||||

RESULT 6
US-10-635-211-4
; Sequence 4, Application US/10635211
; Publication No. US20050031649A1
; GENERAL INFORMATION:
; APPLICANT: Beijing HYDVAX Biotechnology Co. Ltd
; TITLE OF INVENTION: A recombinant fusion protein comprising BCG heat shock protein 65
; TITLE OF INVENTION: and the epitope of MUC1
; FILE REFERENCE: PF03012US
; CURRENT APPLICATION NUMBER: US/10/635,211
; CURRENT FILING DATE: 2003-08-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-635-211-4

Query Match      100.0%; Score 109; DB 17; Length 40;
```

```

Best Local Similarity 100.0%; Pred. No. 4.6e-07; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

Qy 1 GSTAPPAHGVTSPDTRPAP 20
Db 1 GSTAPPAHGVTSPDTRPAP 20

RESULT 7
US-10-106-876-14
; Sequence 14, Application US/10106876
; Publication No. US20030157160A1
; GENERAL INFORMATION:
; APPLICANT: BUDZYNSKI, WLADYSLAW A.
; APPLICANT: KOGANTY, R. RAO
; APPLICANT: KRANTZ, MARK J.
; TITLE OF INVENTION: VACCINE FOR MODULATING BETWEEN T1 AND T2 IMMUNE
; FILE REFERENCE: 042881-0176
; CURRENT APPLICATION NUMBER: US/10/106.876
; PRIOR FILING DATE: 2002-03-27
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-106-876-14

Query Match 100.0%; Score 109; DB 14; Length 43;
Best Local Similarity 100.0%; Pred. No. 5e-07; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

Qy 1 GSTAPPAHGVTSPDTRPAP 20
Db 11 GSTAPPAHGVTSPDTRPAP 30

RESULT 8
US-09-996-069-5
; Sequence 5, Application US/09996069
; Publication No. US20030036199A1
; GENERAL INFORMATION:
; APPLICANT: Bamdad, Cynthia
; APPLICANT: Bamdad, R. Shoshana
; TITLE OF INVENTION: DIAGNOSTIC TUMOR MARKERS, DRUG SCREENING FOR TUMORIGENESIS INHIBITORS AND COMPOSITIONS AND METHODS FOR TREATMENT OF CANCER
; FILE REFERENCE: M01015/70071
; CURRENT APPLICATION NUMBER: US/09/996.069
; PRIOR FILING DATE: 2001-11-27
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-069-5

Query Match 100.0%; Score 109; DB 10; Length 46;
Best Local Similarity 100.0%; Pred. No. 5.4e-07; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

Qy 1 GSTAPPAHGVTSPDTRPAP 20
Db 8 GSTAPPAHGVTSPDTRPAP 27

US-10-106-876-1
; Sequence 1, Application US/10106876
; Publication No. US20030157160A1
; GENERAL INFORMATION:
; APPLICANT: BUDZYNSKI, WLADYSLAW A.
; APPLICANT: KOGANTY, R. RAO
; APPLICANT: KRANTZ, MARK J.
; APPLICANT: LONGENECKER, B. MICHAEL
; TITLE OF INVENTION: VACCINE FOR MODULATING BETWEEN T1 AND T2 IMMUNE
; FILE REFERENCE: 042881-0176
; CURRENT APPLICATION NUMBER: US/10/106.876
; PRIOR FILING DATE: 2002-03-27
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-106-876-1

Query Match 100.0%; Score 109; DB 14; Length 46;
Best Local Similarity 100.0%; Pred. No. 5.4e-07; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

Qy 1 GSTAPPAHGVTSPDTRPAP 20
Db 14 GSTAPPAHGVTSPDTRPAP 33

RESULT 10
US-09-965-131-6
; Sequence 6, Application US/09965131
; Patent No. US20020160502A1
; GENERAL INFORMATION:
; APPLICANT: Chung, Maureen A.
; APPLICANT: Sharma, Surendra
; APPLICANT: Chang, Helena R.
; APPLICANT: O'Donnell, Mark A.
; TITLE OF INVENTION: RECOMBINANT BCG VACCINES FOR THE PREVENTION AND TREATMENT OF CANCER
; FILE REFERENCE: WII-014CP
; CURRENT APPLICATION NUMBER: US/09/965.131
; CURRENT FILING DATE: 2001-09-26
; PRIOR FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-965-131-6

Query Match 100.0%; Score 109; DB 9; Length 100;
Best Local Similarity 100.0%; Pred. No. 1.2e-06; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

Qy 1 GSTAPPAHGVTSPDTRPAP 20
Db 13 GSTAPPAHGVTSPDTRPAP 32

RESULT 11
US-10-635-211-9
; Sequence 9, Application US/10635211
; Publication No. US20050031649A1

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```
; GENERAL INFORMATION:
; APPLICANT: Beijing HYD-VAX Biotechnology Co. Ltd
; TITLE OF INVENTION: A recombinant fusion protein comprising BCG heat shock protein 65
; TITLE OF INVENTION: and the epitope of MUC1
; FILE REFERENCE: FP03012US
; CURRENT APPLICATION NUMBER: US/10/635,211
; CURRENT FILING DATE: 2003-08-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 9
; LENGTH: 159
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion Protein
; US-10-635-211-9

Query Match      100.0%; Score 109; DB 17; Length 159;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSTAPPAHGVTSA PDTRPAP 20
Db 14 GSTAPPAHGVTSA PDTRPAP 33

RESULT 12
US-10-417-312-1
; Sequence 1, Application US/10417312
; Publication No. US20030235868A1
; GENERAL INFORMATION:
; APPLICANT: Dyax Corp
; TITLE OF INVENTION: Antibodies Specific for Mucin Polypeptide
; FILE REFERENCE: 2403/2002
; CURRENT APPLICATION NUMBER: US/10/417,312
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: US 60/374,432
; PRIOR FILING DATE: 2002-04-22
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 1
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-417-312-1

Query Match      100.0%; Score 109; DB 15; Length 475;
Best Local Similarity 100.0%; Pred. No. 5.9e-06;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSTAPPAHGVTSA PDTRPAP 20
Db 129 GSTAPPAHGVTSA PDTRPAP 148

RESULT 13
US-10-636-639-59
; Sequence 59, Application US/10696639
; Publication No. US20050037439A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corporation
; APPLICANT: Bournet, Maureen J.
; TITLE OF INVENTION: DIFFERENTIALLY EXPRESSED GENES INVOLVED IN CANCER, THE
; TITLE OF INVENTION: POLYPEPTIDES ENCODED THEREBY, AND METHODS OF USING THE SAME
; FILE REFERENCE: 01040/1
; CURRENT APPLICATION NUMBER: US/10/696,639
; CURRENT FILING DATE: 2003-10-29
; PRIOR APPLICATION NUMBER: 60/422,176
; PRIOR FILING DATE: 2002-10-29
; NUMBER OF SEQ ID NOS: 3114
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 59
; LENGTH: 475
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```
; TYPE: PRT
; ORGANISM: homo sapiens
; US-10-696-639-59

Query Match      100.0%; Score 109; DB 17; Length 475;
Best Local Similarity 100.0%; Pred. No. 5.9e-06;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSTAPPAHGVTSA PDTRPAP 20
Db 129 GSTAPPAHGVTSA PDTRPAP 148

RESULT 14
US-10-057-136-20
; Sequence 20, Application US/10057136
; Publication No. US20030021770A1
; GENERAL INFORMATION:
; APPLICANT: SCHLOM, JEFFREY
; APPLICANT: KANTOR, JUDITH
; APPLICANT: KUFEL, DONALD
; APPLICANT: PANICALI, DENNIS
; APPLICANT: GRITZ, LINDA
; TITLE OF INVENTION: RECOMBINANT POX VIRUS FOR IMMUNIZATION AGAINST MUC1
; FILE REFERENCE: 700953/47113C
; CURRENT APPLICATION NUMBER: US/10/057,136
; CURRENT FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: 09/366,670
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: PCT/US98/03693
; PRIOR FILING DATE: 1998-02-24
; PRIOR APPLICATION NUMBER: 60/038,253
; PRIOR FILING DATE: 1997-02-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 20
; LENGTH: 508
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-057-136-20

Query Match      100.0%; Score 109; DB 14; Length 508;
Best Local Similarity 100.0%; Pred. No. 6.4e-06;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSTAPPAHGVTSA PDTRPAP 20
Db 76 GSTAPPAHGVTSA PDTRPAP 95

RESULT 15
US-10-635-211-2
; Sequence 2, Application US/10635211
; Publication No. US20050031649A1
; GENERAL INFORMATION:
; APPLICANT: Beijing HYD-VAX Biotechnology Co. Ltd
; TITLE OF INVENTION: A recombinant fusion protein comprising BCG heat shock protein 65
; TITLE OF INVENTION: and the epitope of MUC1
; FILE REFERENCE: FP03012US
; CURRENT APPLICATION NUMBER: US/10/635,211
; CURRENT FILING DATE: 2003-08-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 2
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Recombinant gene
; US-10-635-211-2

Query Match      100.0%; Score 109; DB 17; Length 586;
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Best Local Similarity 100.0%; Pred. No. 7.4e-06;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSTAPPAGHGVTSAPDTRAP 20  
|||  
Db 547 GSTAPPAGHGVTSAPDTRAP 566

Search completed: June 30, 2005, 07:17:59  
Job time : 350 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 30, 2005, 05:30:29 ; Search time 288 Seconds  
(without alignments)  
26.858 Million cell updates/sec

Title: US-10-057-136-1

Perfect score: 109

Sequence: 1 GSTAPPAGVTSAPDTRPAP 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04.\*

1: geneseqp1980s.\*

2: geneseqp1990s.\*

3: geneseqp2000s.\*

4: geneseqp2001s.\*

5: geneseqp2002s.\*

6: geneseqp2003as.\*

7: geneseqp2003bs.\*

8: geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	109	100.0	20	2	AAW77229 Peptide s
2	109	100.0	20	8	ADL15164 Human tum
3	109	100.0	20	8	ADN00795 Human muc
4	109	100.0	26	2	AAW77230 Peptide s
5	109	100.0	27	8	ADN00796 Human muc
6	109	100.0	28	2	AAW03362 Mucin tan
7	109	100.0	30	2	AAW35737 Mucin pep
8	109	100.0	30	2	AAW01781 Synthetic
9	109	100.0	30	4	Aae09543 Human muc
10	109	100.0	31	2	AAW31695 Mucin pep
11	109	100.0	31	6	ABG73816 Tumour-as
12	109	100.0	32	4	Aae09541 Human muc
13	109	100.0	40	2	AAE68002 Mucin rep
14	109	100.0	40	2	AAW54873 Carcinoma
15	109	100.0	40	2	AAW72703 Human muc
16	109	100.0	40	5	ABP56039 Repeat mo
17	109	100.0	40	8	ADP32639 MUC-1 rel
18	109	100.0	41	3	AAV96170 MUC1 repe
19	109	100.0	43	6	AAE33952 Dilipidat
20	109	100.0	43	7	ADD88870 Synthetic
21	109	100.0	46	5	ABP56035 Histidine
22	109	100.0	46	6	AAE33936 MUC 1 pep
23	109	100.0	50	2	AAW35739 Mucin pep
24	109	100.0	51	2	AAW31697 Mucin pep
25	109	100.0	100	5	ABB76181 Synthetic

26	109	100.0	105	2	AAE68022	Aar68022 Mucin pep
27	109	100.0	105	2	AAW72697	Aaw72697 Synthetic
28	109	100.0	173	3	AAV71021	Aay71021 Human muc
29	109	100.0	216	3	AAV92665	Aay92665 MUC-1 ana
30	109	100.0	295	3	AAV71027	Aay71027 Ubiquitin
31	109	100.0	316	8	ADI57755	Adi57755 Human bre
32	109	100.0	325	8	ADI57777	Adi57777 Human bre
33	109	100.0	336	8	ADI57782	Adi57782 Human bre
34	109	100.0	350	8	ADI57754	Adi57754 Human bre
35	109	100.0	372	8	ADI57758	Adi57758 Human bre
36	109	100.0	379	8	ADI57779	Adi57779 Human bre
37	109	100.0	396	8	ADI57776	Adi57776 Human bre
38	109	100.0	398	8	ADI57765	Adi57765 Human bre
39	109	100.0	409	8	ADI57778	Adi57778 Human bre
40	109	100.0	420	8	ADI57770	Adi57770 Human bre
41	109	100.0	455	3	AAV71024	Aay71024 Human muc
42	109	100.0	463	8	ADI57750	Adi57750 Human bre
43	109	100.0	473	4	AAE09508	Aae09508 Human muc
44	109	100.0	475	4	AAU00573	Aau00573 Human MUC
45	109	100.0	475	5	ABB77476	Abb77476 Human MUC

#### ALIGNMENTS

##### RESULT 1

AAW77229

ID AAW77229 standard; peptide; 20 AA.

XX AC AAW77229;

XX DT 20-NOV-1998 (first entry)

XX DE Peptide sequence encoding MUC1 tandem repeat unit.

XX KW MUC1; recombinant pox virus; cytotoxic T-lymphocyte; immunogen; tumour;

XX KW tumour-associated antigen.

XX OS Homo sapiens.

XX PN WO9837095-A2.

XX PD 27-AUG-1998.

XX PF 24-FEB-1998; 98WO-US003693.

XX PR 24-FEB-1997; 97US-0038253P.

XX PA (THER-) THERION BIOLOGICS CORP.

XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX PI (DAND ) DANA FARBEN CANCER INST INC.

XX PI Schlom J, Kantor J, Kufe D, Panicali D, Gritz L;

XX DR WPI; 1998-467492/40.

XX DR N-PSDB; AAV48316.

XX PT New recombinant pox virus for tumour therapy - comprises DNA encoding an

XX PT immunogenic mini-MUC1 fragment comprising 5-25 MUC1 tandem repeat units.

XX PS Example 1; Page 20; 42pp; English.

XX CC The MUC1 tandem repeat unit was used to create an immunogenic mini-MUC1

XX CC fragment for inclusion in a recombinant pox virus (RPV). The RPV was used

XX CC in a pharmaceutical composition also containing an immunomodulator to

XX CC generate MUC1 specific cytotoxic T-lymphocytes. The recombinant pox virus

XX CC therefore encodes an immunogenic MUC1 fragment that does not undergo

XX CC significant genetic deletion, thereby providing an unexpectedly stable

XX CC and immunogenic pox virus. They can be used to prevent or treat tumours

XX CC expressing MUC1 tumour-associated antigens

XX SQ Sequence 20 AA;

```

Query Match      100.0%; Score 109; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5e-07;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSTAPPAGHGVTSAPDTRPAP 20
Db 1 GSTAPPAGHGVTSAPDTRPAP 20

RESULT 2
ID ADL15164 standard; peptide; 20 AA.
AC ADL15164;
DT 17-JUN-2004 (first entry)
DE Human tumour-associated antigen, MUC-1 peptide #1.
KW Therapeutic binding agent; tumour-associated antigen; MUC-1; cancer;
KW tumour; breast carcinoma; colon carcinoma;
KW oesophageal squamous cell carcinoma; pancreatic carcinoma;
KW prostate carcinoma; multiple myeloma; cytostatic; human.
OS Homo sapiens.
XX US6716966-B1.
XX 06-APR-2004.
XX 18-AUG-2000; 2000US-00641833.
XX 18-AUG-1999; 99US-0149492P.
XX 11-NOV-1999; 99US-0164714P.
XX (ALTA-) ALTAREX CORP.
XX Madiyalakan R;
XX WPI; 2004-303095/28.
XX New binding agent, Alt-1, that binds immunological determinants of MUC-1,
XX useful for therapeutically treating a mammal bearing a tumor e.g. breast,
XX colon, esophageal, prostate or pancreatic carcinoma, or multiple myeloma.
XX Disclosure; SEQ ID NO 1; 18pp; English.
XX The present invention relates to therapeutic binding agents that bind to
XX tumour-associated antigen, MUC-1. The binding agent reduces, reverses, or
XX prevents the effects of MUC-1 in cancer. The binding agent is useful for
XX treating a mammal bearing a tumour e.g. breast carcinoma, colon
XX carcinoma, oesophageal squamous cell carcinoma, pancreatic carcinoma,
XX prostate carcinoma or multiple myeloma. The present sequence represents a
XX human MUC-1 peptide.
XX Sequence 20 AA;

Query Match      100.0%; Score 109; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5e-07;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSTAPPAGHGVTSAPDTRPAP 20
Db 1 GSTAPPAGHGVTSAPDTRPAP 20

RESULT 3
ADN00795
ID ADN00795 standard; peptide; 20 AA.
XX ADN00795;
XX 15-JUL-2004 (first entry)

Human mucin 1 (MUC-1) peptide SeqID2.
cell-specific antigen; peripheral blood mononuclear cell;
immunogenic epitope; T lymphocyte; antigen-specific activation;
tumour-specific antigen; human mucin 1; MUC-1; cytostatic;
immunosuppressive; antimicrobial; tumour; adenocarcinomas; HIV infection;
autoimmune disease; infectious disease; human.
Homo sapiens.
WC2004033667-A2.
22-APR-2004.
10-OCT-2003; 2003WO-US032602.
10-OCT-2002; 2002US-0417303P.
(USGO ) US DEPT VETERANS AFFAIRS.
Phillips CA;
WPI; 2004-340926/31.
Detecting and localizing a cell-specific antigen, useful in diagnosing
and treating e.g. tumors, HIV infection, autoimmune disease or infectious
disease, comprises exposing the peripheral blood mononuclear cells to an
immunogenic epitope.
Claim 19; SEQ ID NO 2; 61pp; English.
This invention relates to a novel method of detecting and localising a
cell-specific antigen in a mammal which comprises exposing the peripheral
blood mononuclear cells to a peptide that displays an immunogenic epitope
of the cell-specific antigen under conditions such that T lymphocytes in
the peripheral blood mononuclear cells undergo antigen-specific
activation, thus producing antigen-specific T lymphocytes that bind to
the cell-specific antigen. The cell-specific antigen is preferably a
tumour-specific antigen and the peptide displays an epitope of human
mucin 1 (MUC-1). The invention may be useful for the development of
compounds with a cytostatic, immunosuppressive or antimicrobial activity.
The method is useful in detecting and localising a cell-specific antigen
in a mammal. The method is useful in diagnosing and treating tumours,
particularly adenocarcinomas, HIV infection, autoimmune disease or
infectious disease and in monitoring response to therapy. The present
sequence is that of a human mucin 1 (MUC-1) epitope peptide which may be
used in the method of the invention.
Sequence 20 AA;

Query Match      100.0%; Score 109; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5e-07;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSTAPPAGHGVTSAPDTRPAP 20
Db 1 GSTAPPAGHGVTSAPDTRPAP 20

RESULT 4
AAW77230
ID AAW77230 standard; peptide; 26 AA.
XX AAW77230;
XX 20-NOV-1998 (first entry)
XX Peptide sequence encoding MUC1 tandem repeat unit a.
XX MUC1; recombinant pox virus; cytotoxic T-lymphocyte; immunogen; tumour;
XX tumour-associated antigen.

```



PT derived from longer template peptide, useful as pharmaceutical or vaccine  
 PT against infectious disease or malignancy.

XX Claim 9; Page 36; 60pp; English.

XX The present peptide contains a mucin tandem repeat, which elicits non-MHC  
 CC restricted cytotoxic T lymphocyte responses, and can be used as a  
 CC template in the prepn. of a ratchet library, comprising peptides contg.  
 CC at least 1 immunostimulatory CTL epitope. Basically the distribution of  
 CC amino acids at each position in the template is calculated, a ratchet  
 CC library constructed from the longer template peptide by sequentially  
 CC ratcheting it into the shorter ratchet length and the peptides  
 CC synthesised using standard solid phase methods. The library can be used  
 CC in pharmaceuticals and vaccines for the treatment, and/or prevention of  
 CC disease and malignancy associated with mucin secretion, e.g. cancer.  
 CC Several epitopes can be incorporated into the same library, rather than  
 CC using a mixt. of individually synthesised immunogenic peptides, which  
 CC helps to overcome problems of genetic diversity and MHC restriction. The  
 CC library may also include antigenic variations and escape mutations  
 XX  
 SQ Sequence 28 AA;

Query Match 100.0%; Score 109; DB 2; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-07;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSTAPPAGVTSAPDTRPAP 20  
 |||||  
 Db 8 GSTAPPAGVTSAPDTRPAP 27

RESULT 7  
 AAW35737  
 ID AAW35737 standard; peptide; 30 AA.

XX  
 AC AAW35737;

DT 02-APR-1998 (first entry)

XX Mucin peptide MUC1-3.

XX MUC1; mucin; vaccine; keyhole limpet haemocyanin; KHL; cancer;  
 KW immunogenic protein, immune response.

XX Synthetic.

OS Mammalia.

XX WO9734921-A1.

XX 25-SEP-1997.

XX 20-MAR-1997; 97WO-US004493.

XX 20-MAR-1996; 96US-0013775P.

XX (SLOK) SLOAN KETTERING INST CANCER RES.

XX Livingston PO, Zhang S;

XX WPI; 1997-480158/44.

XX Vaccine effective against cancer of the breast, prostate, colon, lung or  
 PT pancreas - comprising mucin peptide, especially MUC1, conjugated to  
 PT immunogenic protein, especially keyhole limpet haemocyanin.

XX Claim 7; Page 38; 45pp; English.

XX This mucin peptide is used in a vaccine capable of producing an immune  
 CC response which recognises a mucin. The mucin peptide is selected from  
 CC MUC1 peptide group. The vaccine comprises an amount of the mucin peptide  
 CC conjugated to an immunogenic protein effective to stimulate or enhance  
 CC immune response in the subject, together with an adjuvant and a vehicle.  
 CC The immunogenic protein is a keyhole limpet haemocyanin (KHL) or its

CC derivative. The vaccine can be used to induce an immune response in  
 CC patients suffering from a cancer of the type where the cancer cells have  
 CC mucin on their surface, e.g. breast cancer, prostate cancer, lung cancer,  
 CC colon cancer or pancreas cancer

XX Sequence 30 AA;

Query Match 100.0%; Score 109; DB 2; Length 30;

Best Local Similarity 100.0%; Pred. No. 2.3e-07;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSTAPPAGVTSAPDTRPAP 20  
 |||||  
 Db 9 GSTAPPAGVTSAPDTRPAP 28

RESULT 8

AAW01781

ID AAW01781 standard; peptide; 30 AA.

XX AC AAW01781;

XX 20-AUG-1997 (first entry)

XX Synthetic MUC1 antigen SPI-070.

XX T cell antigen epitope; Th1 specific immunomodulator; ovarian cancer;  
 KW tuberculosis; malaria; breast cancer; pancreatic cancer;  
 KW respiratory syncytial virus infection; leishmaniasis; leprosy;  
 KW candidiasis.

XX Synthetic.

XX WO9640066-A1.

XX 19-DEC-1996.

XX 07-JUN-1996; 96WO-US009951.

XX 07-JUN-1995; 95US-00480499.

XX (UVAL-) UNIV ALBERTA.

XX Samuel J, Kwon GS;

XX WPI; 1997-051816/05.

XX Compon. contg. T cell antigen epitope and Th1 specific immuno:modulator -  
 PT useful for eliciting Th1 specific immune response to treat e.g. cancer,  
 PT tuberculosis, malaria, etc.

XX Example 1; Page 30; 79pp; English.

XX A novel composition is able to elicit Th1 type immune responses against  
 CC short T-cell epitope-containing peptides without the use of traditional  
 CC carrier proteins and immunoadjuvants. The composition involves: a slow  
 CC release vehicle; an immunogenically effective amount of a synthetic  
 CC peptide consisting of an 11-14 amino acid sequence containing at least  
 CC one T cell antigen epitope; and an immunogenically effective amount of a  
 CC Th1 specific immunomodulator. The present sequence is synthetic MUC1  
 CC antigen SPI-070, which was used as an example of an amino acid sequence  
 CC in the new composition and produced strong proliferation (24 to 71 fold  
 CC above background). The composition can be used to elicit a Th1 specific  
 CC immune response, preferably a protective immune response, to treat e.g.  
 CC breast, pancreatic and ovarian cancer, respiratory syncytial virus  
 CC infections, leishmaniasis, malaria, tuberculosis, leprosy and candidiasis

XX Sequence 30 AA;

Query Match 100.0%; Score 109; DB 2; Length 30;

Best Local Similarity 100.0%; Pred. No. 2.3e-07;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY      1  GSTAPPAGHGVTSAPDTRPAP 20
Db      5  GSTAPPAGHGVTSAPDTRPAP 24

RESULT 9
AAE09543
ID  AAE09543 standard; peptide; 30 AA.
XX
AC  AAE09543;
XX
DT      19-NOV-2001 (first entry)
XX
DE  Human mucin-1 (MUC-1) extracellular epitope #14 for CTL.
XX
KW  Mucin-1; cytostatic; immunostimulant; cell mediated immune response;
KW  carcinoma; adenocarcinoma; breast cancer; dendritic cell; vaccine;
KW  gene therapy; human; MUC-1; cytotoxic T-lymphocyte; CTL.
XX
OS  Homo sapiens.
XX
PN  WO200157068-A1.
XX
PD      09-AUG-2001.
XX
PF      01-FEB-2001; 2001WO-AU0000090.
XX
PR      01-FEB-2000; 2000AU-00005369.
PR      14-JUN-2000; 2000US-00593870.
XX
PA  (AUST-) AUSTIN RES INST.
XX
PI  McKenzie IFC, Pietersz GA, Apostolopoulos V;
XX
DR  WPI; 2001-541537/60.
XX
KW  Immunostimulant peptide, used as an anti-carcinoma vaccine, comprises a
PT  an epitope of the non-VNTR, non-leader region of a mucin.
XX
PS  Disclosure; Page 34; 84pp; English.
XX
CC  The patent discloses peptide or polypeptides capable of eliciting an
CC  immune response, comprising an amino acid sequence corresponding to an
CC  epitope of the non-central portion of varying numbers of an amino acid
CC  motif (VNTR), non-leader region of a mucin. The peptides of the
CC  invention, fusion proteins comprising the peptide and conjugate compounds
CC  with carbohydrate polymers are used to induce a cell mediated immune
CC  response against mucin in the prevention or treatment of carcinoma,
CC  preferably adenocarcinoma, most preferably breast cancer. They are also
CC  used to pulse dendritic cell for in vivo transfer and use as a vaccine.
CC  They are also used in gene therapy. The present sequence is an
CC  extracellular peptide of mucin-1 (MUC-1) protein from human. This
CC  sequence is an epitope for cytotoxic T-lymphocytes (CTL)
XX
SQ  Sequence 30 AA;

Query Match      100.0%; Score 109; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.3e-07;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GSTAPPAGHGVTSAPDTRPAP 20
Db      8  GSTAPPAGHGVTSAPDTRPAP 27

RESULT 10
AAW31695
ID  AAW31695 standard; peptide; 31 AA.
XX
AC  AAW31695;
XX
DT      02-APR-1998 (first entry)
XX
DE  Tumour-associated antigen mucin-1 (MUC1) peptide, E31-biotin.
XX
KW  Human; MUC1; mucin-1; cytostatic; antagonist; vaccine; tumour;
KW  tumour-associated mucin-1; cancer; breast carcinoma; colon carcinoma;
KW  oesophageal squamous cell carcinoma; pancreatic carcinoma;
KW  prostate carcinoma; multiple myeloma; adenocarcinoma.
XX
OS  Homo sapiens.
XX
PN  Key      Location/Qualifiers
XX      1..8
XX      /label= Type_1_turn
XX      2..6
XX      /label= T_cell_epitope

```

Mucin peptide MUC1-3 with C-terminal cysteine.

MUC1; mucin; vaccine; keyhole limpet haemocyanin; KHL; cancer; immunogenic protein; immune response; conjugate.

Synthetic.

Mammalia.

WO9734921-A1.

25-SEP-1997.

20-MAR-1997; 97WO-US004493.

20-MAR-1996; 96US-0013775P.

(SLOK ) SLOAN KETTERING INST CANCER RES.

Livingston PO, Zhang S;

WPI; 1997-480158/44.

Vaccine effective against cancer of the breast, prostate, colon, lung or pancreas - comprising mucin peptide, especially MUC1, conjugated to immunogenic protein, especially keyhole limpet haemocyanin.

Disclosure; Page 11; 45pp; English.

This mucin peptide is used in a vaccine capable of producing an immune response which recognises a mucin. The mucin peptide is selected from MUC1 peptide group. The vaccine comprises an amount of the mucin peptide conjugated to an immunogenic protein effective to stimulate or enhance immune response in the subject, together with an adjuvant and a vehicle. A cysteine is added to the C-terminal of this peptide to facilitate the conjugation with protein carriers. The immunogenic protein is a keyhole limpet haemocyanin (KLH) or its derivative. The vaccine can be used to induce an immune response in patients suffering from a cancer of the type where the cancer cells have mucin on their surface, e.g. breast cancer, prostate cancer, lung cancer, colon cancer or pancreas cancer

Sequence 31 AA;

Query Match 100.0%; Score 109; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 2.4e-07;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSTAPPAGHGVTSAPDTRPAP 20
Db 9 GSTAPPAGHGVTSAPDTRPAP 28

RESULT 11
ABG73816
ID ABG73816 standard; peptide; 31 AA.
XX
AC ABG73816;
XX
DT 20-MAR-2003 (first entry)
XX
DE Tumour-associated antigen mucin-1 (MUC1) peptide, E31-biotin.
XX
KW Human; MUC1; mucin-1; cytostatic; antagonist; vaccine; tumour;
KW tumour-associated mucin-1; cancer; breast carcinoma; colon carcinoma;
KW oesophageal squamous cell carcinoma; pancreatic carcinoma;
KW prostate carcinoma; multiple myeloma; adenocarcinoma.
XX
OS Homo sapiens.
XX
PN Key Location/Qualifiers
XX 1..8
XX /label= Type\_1\_turn
XX 2..6
XX /label= T\_cell\_epitope

Region 3. .8  
/label= Alt-1 epitope  
/note= "Alt-1 is a TSA-specific murine monoclonal antibody. Residues 3-8 specifically claimed in claim 34"

Region 7. .12  
/label= Epitope\_region

Region 9. .28  
/label= MUC1 extracellular domain core  
/note= "MUC1 extracellular domain consists of 30 to 90 tandem repeats of this sequence"

Region 11. .16  
/label= Epitope\_region

Region 15. .20  
/label= Epitope\_region

Region 19. .24  
/label= Epitope\_region

Region 20. .26  
/label= B\_cell epitope

Region 21. .28  
/label= Type\_1\_turn

Region 22. .26  
/label= T\_cell epitope

Region 23. .28  
/label= Alt-1 epitope  
/note= "Alt-1 is a TSA-specific murine monoclonal antibody. Residues 3-8 specifically claimed in claim 34"

Modified-site 31  
/note= "Biotinylated"

US2002132771-A1.

19-SEP-2002.

26-NOV-2001; 2001US-00994466.

18-AUG-1999; 99US-0149492P.

11-NOV-1999; 99US-0164714P.

18-AUG-2000; 2000US-00641833.

28-NOV-2000; 2000US-00724094.

21-FEB-2001; 2001US-0270456P.

21-FEB-2001; 2001US-0270471P.

(MADI/) MADIYALAKAN R.

Madiyalakan R;

WPI; 2003-155898/15.

New therapeutic compositions comprising a binding agent that binds to tumor-associated MUC1 epitope, useful for treating human tumors, e.g. breast carcinoma, prostate carcinoma or multiple myeloma.

Example 24; Page 13; 27pp; English.

The invention relates to new therapeutic compositions, which comprise a binding agent that specifically binds to an epitope of a tumour-associated mucin-1 (MUC1), are effective for treating a mammal bearing a tumour. Mice were implanted with 413BCR tumour cells 2 weeks after the start of the immunisation series (using either a conjugate of the binding agent, or a complex of the binding agent-MUC1). It was found that a humoral response was induced in mice treated with both the conjugated and complexed binding agent. A T2 cellular response to the binding agent was induced in these mice. A trend for reduction in tumour mass and size in mice treated with the conjugated or complexed binding agent was also demonstrated. The therapeutic compositions or the method is useful for treating a mammal (particularly a human) bearing a tumour, especially a tumour that expresses a tumour-associated MUC-1. In particular, the compositions are useful for treating adenocarcinomas, e.g. breast carcinoma, colon carcinoma, oesophageal squamous cell carcinoma, pancreatic carcinoma, prostate carcinoma, or multiple myeloma. The present sequence represents the mucin-1 peptide, E31-biotin

Sequence 31 AA;

Query Match 100.0%; Score 109; DB 6; Length 31;  
Best Local Similarity 100.0%; Pred. No. 2.4e-07;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSTAPPAHGVTSPDTRPAP 20  
|||||  
Db 9 GSTAPPAHGVTSPDTRPAP 28  
|||||

RESULT 12  
AAE09541  
ID AAE09541 standard; peptide; 32 AA.  
XX  
AC AAE09541;  
XX  
XX 19-NOV-2001 (first entry)  
XX  
DE Human mucin-1 (MUC-1) VNTR peptide #5.  
XX  
KW Mucin-1; cytostatic; immunostimulant; cell mediated immune response;  
KW carcinoma; adenocarcinoma; breast cancer; dendritic cell; vaccine;  
KW gene therapy; human; MUC-1.  
XX  
OS Homo sapiens.  
XX  
PN WO200157068-A1.  
XX  
PD 09-AUG-2001.  
XX  
XX 01-FEB-2001; 2001WO-AU000090.  
XX  
PF 01-FEB-2000; 2000AU-00005369.  
PR 14-JUN-2000; 2000US-00593870.  
XX  
XX  
PA (AUST-) AUSTIN RES INST.  
XX  
XX McKenzie IFC, Pietersz GA, Apostolopoulous V;  
XX  
XX WPI; 2001-541537/60.  
XX  
PT Immunostimulant peptide, used as an anti-carcinoma vaccine, comprises a  
PT an epitope of the non-VNTR, non-leader region of a mucin.  
XX  
PS Disclosure; Page 34; 84pp; English.  
XX  
CC The patent discloses peptide or polypeptides capable of eliciting an  
CC immune response, comprising an amino acid sequence corresponding to an  
CC epitope of the non-central portion of varying numbers of an amino acid  
CC motif (VNTR), non-leader region of a mucin. The peptides of the  
CC invention, fusion proteins comprising the peptide and conjugate compounds  
CC with carbohydrate polymers are used to induce a cell mediated immune  
CC response against mucin in the prevention or treatment of carcinoma,  
CC preferably adenocarcinoma, most preferably breast cancer. They are also  
CC used to pulse dendritic cell for in vivo transfer and use as a vaccine.  
CC They are also used in gene therapy. The present sequence is a VNTR  
CC peptide of mucin-1 (MUC-1) protein from human  
XX  
SQ Sequence 32 AA;

Query Match 100.0%; Score 109; DB 4; Length 32;  
Best Local Similarity 100.0%; Pred. No. 2.4e-07;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSTAPPAHGVTSPDTRPAP 20  
|||||  
Db 8 GSTAPPAHGVTSPDTRPAP 27  
|||||

RESULT 13  
AAR68002  
ID AAR68002 standard; peptide; 40 AA.  
XX

```

AC AAR68002;
XX
XX 25-MAR-2003 (revised)
DT 05-SEP-1995 (first entry)
XX
XX Mucin repeat sequence.
DE
XX
XX Mucin; multiple tandem repeat; vaccine; pancreas cancer; breast cancer;
KW ovary cancer; colon cancer; HIV.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH Region 3..5
FT /label= DTR motif
FT /note= "can be substituted by viral sequence, tumor
FT antigen or autoantigen"
XX
XX
XX WO9503825-A1.
XX
XX 09-FEB-1995.
PD
XX
XX 29-JUL-1994; 94WO-US008477.
XX
XX 30-JUL-1993; 93US-00099354.
XX
XX (FINN/) FINN O J.
PA (FONT/) FONTENOT J D.
PA (MONT/) MONTELLARO R C.
XX
XX Finn OJ, Fontenot JD, Montelaro RC;
PI
XX
XX WPI; 1995-082033/11.
XX
XX Synthetic multiple tandem repeat mucin-1 peptides and analogues - have
PT native conformation in the absence of glycosylation and are linked to
PT epitopes; for vaccines and tests of cancer, viruses and bacteria.
XX
XX Disclosure; Page 32; 125pp; English.
XX
XX A synthetic peptide comprises at least 4 tandem repeats of the mucin
CC peptide given in (AAR68002). The multiple prolines of the repeat
CC structure are needed to maintain a rigid structure. The DTR motif,
CC located between the first 2 prolines in each repeat, is the target of an
CC anti-mucin immune response, and can be substituted by a sequence from a
CC virus, tumor antigen or autoantigen, for use in vaccine development.
XX (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 40 AA;
SQ
Query Match 100.0%; Score 109; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 3e-07;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GSTAPPAGVTSAPDTRPAP 20
Db 9 GSTAPPAGVTSAPDTRPAP 28
RESULT 14
AAW54873
ID AAW54873 standard; peptide; 40 AA.
XX
XX AAW54873;
AC
XX
XX 24-SEP-1998 (first entry)
DT
XX
XX Carcinoma-associated antigen DP3/MUC1 tandem repeat segment.
DE
XX
XX Mucin; DP3/MUC1; cytotoxic T lymphocyte; autoimmune disease;
KW granuloma formation; transplant rejection.
XX
XX Homo sapiens.
OS

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XX WO9817300-A1.
XX
XX 30-APR-1998.
XX
XX 24-OCT-1997; 97WO-US019784.
XX
XX 25-OCT-1996; 96US-00738262.
XX
XX (DAND ) DANA FARBER CANCER INST INC.
XX
XX Gong J, Kufe D;
XX
XX WPI; 1998-261182/23.
XX
XX Use of tandem repeat segment of mucin - as target for modulating effects
PT of cytotoxic T lymphocytes in the treatment of e.g. autoimmune disease,
PT transplant rejection or tumours.
XX
XX Disclosure; Page 28; 45pp; English.
XX
XX The tandem repeat segment of a mucin such as DP3/MUC1 can be used in an
CC in vivo method for decreasing or preventing the deleterious effects of
CC cytotoxic T lymphocytes (CTLs) in an animal. It can be used to treat
CC disorders characterised by activation of CTLs, such as autoimmune
CC diseases (e.g. diabetes, lupus and multiple sclerosis) and conditions
CC characterised by CTL induced granuloma formation, e.g. tuberculosis,
CC sarcoidosis, leprosy, Crohn's disease, hypersensitivity pneumonitis, and
CC primary biliary cirrhosis. The methods can also be used to treat
CC transplant rejection and malignant disorders of CTLs, e.g. activated T
CC cell leukaemia/lymphoma
XX
XX Sequence 40 AA;
SQ
Query Match 100.0%; Score 109; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 3e-07;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GSTAPPAGVTSAPDTRPAP 20
Db 12 GSTAPPAGVTSAPDTRPAP 31
RESULT 15
AAW72703
ID AAW72703 standard; peptide; 40 AA.
XX
XX AAW72703;
AC
XX
XX 11-JAN-1999 (first entry)
DT
XX
XX Human mucin peptide.
DE
XX
XX Mucin; muc-1; human; cancer; infectious disease; vaccine; diagnosis;
KW multiple tandem repeat; pancreatic cancer; breast cancer; colon cancer.
XX
XX Homo sapiens.
OS
XX
XX US5827666-A.
PN
XX
XX 27-OCT-1998.
PD
XX
XX 10-AUG-1994; 94US-00288059.
XX
XX 30-JUL-1993; 93US-00099354.
XX
XX (UYPI-) UNIV PITTSBURGH.
XX
XX Montelaro RC, Fontenot JD, Finn OJ;
PI
XX
XX WPI; 1998-593988/50.
XX
XX Assay for cancer antibodies - using synthetic peptide comprising multiple
PT

```

PT tandem repeats of muc-1.  
 XX  
 PS Disclosure; Col 15; 45pp; English.  
 XX  
 CC An assay has been developed for antibodies to pancreatic, breast or colon  
 CC cancer in a sample. The assay comprises contacting the sample with a  
 CC synthetic muc-1 peptide that comprises at least two 20 amino acid tandem  
 CC repeats of muc-1 and is capable of attaining native conformation in the  
 CC absence of glycosylation, and detecting any peptide-antibody complex  
 CC formation. The assay can be used in the diagnosis of e.g. pancreatic,  
 CC breast or colon cancer. The present sequence represents a human mucin  
 CC peptide from the present invention  
 XX  
 SQ Sequence 40 AA;  
 Query Match 100.0%; Score 109; DB 2; Length 40;  
 Best Local Similarity 100.0%; Pred. No. 3e-07;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GSTAPPAGVTSAPDTRPAP 20  
 |||||  
 Db 9 GSTAPPAGVTSAPDTRPAP 28  
 |||||

Search completed: June 30, 2005, 06:42:55  
 Job time : 289 secs